

153107

Schreiber, David

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From: Angell, Jon E  
Sent: Wednesday, May 04, 2005 4:53 PM  
To: ~~Schreiber, David~~  
Subject: SPDI Sequence Database Search Request 09/978,375 SPDI

SEARCH REQUEST FORM  
Scientific and Technical Information Center

Examiner# : 78697  
Art Unit : 1635  
Phone Number: 571-272-0756  
Date: 5/4/05  
Serial Number: 09/978,375  
Mailbox & Bldg/Room Location: REMSEN 2C18  
Results Format Preferred (circle): Paper

***This case is a SPDI Application***

I would like to have a search performed (commercial and interference databases) using the following SEQ. ID NOS. from application : 09/978,375

SEQ ID NO. 59 (amino acid ~ 373 amino acids long)

Please search the PROTEIN databases using SEQ ID NO: 59

NOTE: The sequence of this application is also related to the sequences of 09/978,544 and 10/002,967 (search requests for these apps are being submitted immediately after this request)

Please don't hesitate to call if you need clarification for any request

Thanks,  
Eric

J. Eric Angell  
Art Unit 1635  
REMSSEN 2D20  
571-272-0756

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## Scientific and Technical Information Center

## SEARCH REQUEST FORM

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
 Art Unit: \_\_\_\_\_ Phone Number: 2- \_\_\_\_\_ Serial Number: \_\_\_\_\_  
 Location (Bldg/Room#): \_\_\_\_\_ (Mailbox #): \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK  
 \*\*\*\*\*

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Date: \_\_\_\_\_

## Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

## STAFF USE ONLY

Searcher: D. Schweiden

Searcher Phone #: 272-2526

Searcher Location: Rensen E01 A61

Date Searcher Picked Up: \_\_\_\_\_

Date Completed: 5/11

Searcher Prep & Review Time: 15

Online Time: 16

## Type of Search

\_\_\_\_\_ NA Sequence (#)

1 AA Sequence (#)

\_\_\_\_\_ Structure (#)

\_\_\_\_\_ Bibliographic

\_\_\_\_\_ Litigation

\_\_\_\_\_ Fulltext

\_\_\_\_\_ Other

## Vendors and cost where applicable

\_\_\_\_\_ STN \_\_\_\_\_ Dialog

\_\_\_\_\_ Questel/Orbit \_\_\_\_\_ Lexis/Nexis

\_\_\_\_\_ Westlaw \_\_\_\_\_ WWW/Internet

☒ In-house sequence systems CompuGen

☒ Commercial \_\_\_\_\_ Oligomer \_\_\_\_\_ Score/Length

☒ Interference ☒ SPDI \_\_\_\_\_ Encode/Transl

\_\_\_\_\_ Other (specify)

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GenCore version 5.1.6

OM protein - protein search, using sw model  
Run on: May 5, 2005, 08:03:49; Search time 164 Seconds  
(without alignments)  
879.644 Million cell updates/sec

Title: US-09-978-375A-59

Perfect score: 1908

Sequence: 1 MSLLLLLLVSVYVGLGTH.....TKAETTPSMIPQSRAFQTV 373

Scoring table: BLOSUM62

Gap: 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database: A\_Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003s:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No. Score Match Length DB ID

RESULT 1

ID AAY41692 standard; protein; 373 AA.

DE Human PRO 363 protein sequence.

PN WO9946281-A2.

PD 16-SEP-1999.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1908; DB 2; Length 373;

Best Local Similarity 100.0%; Pred. No. 3.7e-145;

RESULT 2

ID AAB33430 standard; protein; 373 AA.

DE Human PRO363 protein UNQ318 SEQ ID NO:87.

PN WO200053758-A2.

PD 14-SEP-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1908; DB 3; Length 373;

Best Local Similarity 100.0%; Pred. No. 3.7e-145;

RESULT 3

ID AAB44248 standard; protein; 373 AA.

DE Human PRO363 (UNQ318) protein sequence SEQ ID NO:59.

PN WO200053756-A2.

PD 14-SEP-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1908; DB 3; Length 373;

Best Local Similarity 100.0%; Pred. No. 3.7e-145;

RESULT 4

ID AAU12365 standard; protein; 373 AA.

DE Human PRO363 polypeptide sequence.

PN WO200140466-A2.

PD 07-JUN-2001.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1908; DB 4; Length 373;

Best Local Similarity 100.0%; Pred. No. 3.7e-145;

RESULT 5

ID AAB48108 standard; protein; 373 AA.

DE Human A236 polypeptide.

PN WO200069885-A2.

PD 23-NOV-2000.

PA (MILL-) MILLENNIUM PHARM INC.

Query Match 100.0%; Score 1908; DB 4; Length 373;

Best Local Similarity 100.0%; Pred. No. 3.7e-145;

RESULT 6

ID AAB65293 standard; protein; 373 AA.

DE Novel human secreted or transmembrane protein PRO363.

PN US2002132252-A1.

DE Human PRO363 protein sequence SEQ ID NO:503.  
PN WO200073454-A1.

PD 07-DEC-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1908; DB 4; Length 373;

Best Local Similarity 100.0%; Pred. No. 3.7e-145;

RESULT 7

ID AAU83656 standard; protein; 373 AA.

DE Human PRO protein, Seq ID No 130.

PN WO200208288-A2.

PD 31-JAN-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1908; DB 5; Length 373;

Best Local Similarity 100.0%; Pred. No. 3.7e-145;

RESULT 8

ID ABB84848 standard; protein; 373 AA.

DE Human PRO363 protein sequence SEQ ID NO:64.

PN WO20020690-A2.

PD 03-JAN-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1908; DB 5; Length 373;

Best Local Similarity 100.0%; Pred. No. 3.7e-145;

RESULT 9

ID AAE26448 standard; protein; 373 AA.

DE Human A236 protein.

PN US2002055139-A1.

PD 09-MAY-2002.

PA (HOLT/) HOLTZMAN D A.

PA (SHAR/) SHARP J D.

PA (LEIB/) LEIBY K R.

PA (BOSS/) BOSSOME S.

PA (PANY/) PAN Y.

PA (BARN/) BARNES T M.

PA (FRAS/) FRASER C C.

PA (WRIG/) WRIGHTON N.

PA (MYER/) MYERS P S.

PA (KING/) KINGSBURY G.

Query Match 100.0%; Score 1908; DB 5; Length 373;

Best Local Similarity 100.0%; Pred. No. 3.7e-145;

RESULT 10

ID ABB95454 standard; protein; 373 AA.

DE Human angiogenesis related protein PRO363 SEQ ID NO: 64.

PN WO200208284-A2.

PD 31-JAN-2002.

PA (GETH) GENENTECH INC.

PA (BAKE/) BAKER K P.

PA (FERR/) FERRARA N.

PA (GERB/) GERBER H.

PA (GERR/) GERRITSEN M E.

PA (GODD/) GODDARD A.

PA (GODO/) GODOWSKI P J.

PA (GURN/) GURNEY A L.

PA (HILL/) HILLAN K J.

PA (MARS/) MARSTERS S A.

PA (PANJ/) PAN J.

PA (PAON/) PAONI N F.

PA (STEP/) STEPHAN J F.

PA (WATA/) WATANABE C K.

PA (WILL/) WILLIAMS P M.

PA (WOOD/) WOOD W I.

Query Match 100.0%; Score 1908; DB 5; Length 373;

Best Local Similarity 100.0%; Pred. No. 3.7e-145;

RESULT 11

ID ABUS8108 standard; protein; 373 AA.

DE Human PRO polypeptide #140.

PN US2003027163-A1.

PD 06-FEB-2003.

Query Match 100.0%; Score 1908; DB 6; Length 373;

Best Local Similarity 100.0%; Pred. No. 3.7e-145;

RESULT 12

ID ABUS9186 standard; protein; 373 AA.

DE Novel human secreted or transmembrane protein PRO363.

PN US2002132252-A1.

PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 13  
ID ABU82698 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein PRO363.  
PN US2003032023-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 14  
ID ABO17809 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003032156-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 15  
ID ABU60617 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein, #176.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 16  
ID ABU80803 standard; protein; 373 AA.  
DE Human PRO polypeptide #65.  
PN US2003036635-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 17  
ID ABO25194 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003050239-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 18  
ID ABO33769 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003045687-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 19  
ID ABU1999 standard; protein; 373 AA.  
DE Human PRO363 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 20  
ID ABU81063 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003004311-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 21  
ID ABU72200 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2002192706-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 22  
ID ABU72584 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003003531-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 23  
ID ABU66763 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003036180-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 24  
ID ABU84880 standard; protein; 373 AA.  
DE Human secreted and transmembrane polypeptide PRO363.  
PN US200217553-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 25  
ID ABUS9844 standard; protein; 373 AA.  
DE Novel secreted and transmembrane protein PRO363.  
PN US2003017563-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 26  
ID ABU61078 standard; protein; 373 AA.  
DE Human PRO363 polypeptide.  
PN US2002169284-A1.  
PD 14-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 27  
ID ABUS9333 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein, #176.  
PN US2003027182-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 28  
ID ABO26030 standard; protein; 373 AA.  
DE Human PRO363 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 29  
ID ABO25034 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein (PRO) #194.  
PN US2003036179-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 30  
ID ABU80347 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein PRO363.  
PN US2003004102-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;

RESULT 31  
ID ABU82112 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003088063-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 32  
ID ABU59039 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein, #176.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 33  
ID ABU92417 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 34  
ID ABU59482 standard; protein; 373 AA.  
DE Novel human secreted or transmembrane protein PRO5723.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 35  
ID ABU67039 standard; protein; 373 AA.  
DE Human secreted/transmembrane, PRO, protein SEQ ID 388.  
PN US2003032155-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 36  
ID ABU92248 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 37  
ID ABU10954 standard; protein; 373 AA.  
DE Human PRO polypeptide #140.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 38  
ID ABU81706 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 39  
ID ABU88645 standard; protein; 373 AA.  
DE Human secreted and transmembrane polypeptide PRO363.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 40  
ID ABO34159 standard; protein; 373 AA.  
DE Human PRO363 polypeptide.  
PN US2003017981-A1.

PD 23-JAN-2003.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 41  
ID ADA45907 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003022328-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 42  
ID ADA76338 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003073212-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 43  
ID ABJ72292 standard; protein; 373 AA.  
DE Human PRO363 protein.  
PN US2003050448-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 44  
ID ADA18988 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003054517-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 45  
ID ADA61611 standard; protein; 373 AA.  
DE Homo sapiens.  
PN US2003049816-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 46  
ID ADB19396 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003068796-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 47  
ID ADB27937 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003082704-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 48  
ID ADA86416 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003082711-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 49  
ID ADB15980 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003087350-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 50  
ID ADA38014 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein PRO363.  
PN US200308297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 51  
ID ADA47766 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003073215-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 52  
ID ADA21700 standard; protein; 373 AA.  
DE Human secreted/transmembrane polypeptide PRO363.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 53  
ID ADA10487 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein, PRO363.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 54  
ID ADA67561 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003068795-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 55  
ID ADB30568 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003068794-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 56  
ID ADA85864 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003082693-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 57  
ID ADA18031 standard; protein; 373 AA.  
DE Human PRO363 polypeptide.  
PN US2003054987-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 58  
ID ADA97076 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003082705-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 59  
ID ADA79380 standard; protein; 373 AA.

DE Human PRO polypeptide #194.  
PN US2003082763-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 60  
ID ADA87519 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003087345-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 61  
ID ADB16721 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003087349-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 62  
ID ADA28139 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein PRO363.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 63  
ID ADA91813 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003082694-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 64  
ID ADB14876 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003087351-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 65  
ID ADA24598 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003050241-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 66  
ID ADB18837 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003073211-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 67  
ID ADA94052 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003077722-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 68  
ID ADB19948 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003082691-A1.

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PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 69
ID ADB13260 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 70
ID ADA43342 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 71
ID ABO19649 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 72
ID ADA12259 standard; protein; 373 AA.
DE Human secreted/transmembrane polypeptide PRO363.
PN US200305216-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 73
ID ADA94719 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 74
ID ADA74514 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 75
ID ADB24747 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 76
ID ADA82271 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 77
ID ADA75234 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 78
ID ADA85312 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 79
ID ADA84760 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 80
ID ADB30016 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 81
ID ADA80544 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 82
ID ADA75786 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 83
ID ADA38944 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 84
ID ADA47011 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 85
ID ADB25307 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 86
ID ADA93483 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 87
ID ADA75234 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
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RESULT 87  
ID ADB26833 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003092147-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 88  
ID ADB31120 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003096386-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 89  
ID ABJ72420 standard; protein; 373 AA.  
DE Human PRO363 protein.  
PN US2003027988-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 90  
ID ADA93065 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein PRO363.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 91  
ID ADA61048 standard; protein; 373 AA.  
DE Homo sapiens.  
PN US2003049817-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 92  
ID ADB24195 standard; protein; 373 AA.  
DE Human PRO polypeptide SEQ ID NO 388.  
PN US2003077714-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 93  
ID ADA96524 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003082690-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 94  
ID ADA81096 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003082702-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 95  
ID ADA95972 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003082759-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 96  
ID ADB26281 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003082699-A1.

DE Human PRO polypeptide #194.  
PN US2003082760-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 97  
ID ADB21766 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003082765-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 98  
ID ABO34315 standard; protein; 373 AA.  
DE Human secreted/transmembrane polypeptide PRO 363.  
PN US2003044934-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 99  
ID ABO19540 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane polypeptide #8.  
PN US2003049633-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 6; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 100  
ID ADA77545 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003068797-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 101  
ID ADB18285 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003077710-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 102  
ID ADA86968 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003082709-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 103  
ID ADA88071 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003082700-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 104  
ID ADA6459 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003054516-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 105  
ID ADB28489 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003082699-A1.

PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;  
RESULT 106  
ID ADB25041 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003082706-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;  
RESULT 107  
ID ABO53245 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein PRO363.  
PN US2003044806-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;  
RESULT 108  
ID ADA76993 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003059909-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;  
RESULT 109  
ID ADA22626 standard; protein; 373 AA.  
DE Human secreted/transmembrane polypeptide PRO363.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;  
RESULT 110  
ID ADA88623 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003073213-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;  
RESULT 111  
ID ADA97628 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003082686-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;  
RESULT 112  
ID ADB27385 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US200302239-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;  
RESULT 113  
ID ADB22318 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003087344-A1.  
PD 08-MAY-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;  
RESULT 114  
ID ABO22615 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein PRO363.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;  
RESULT 115  
ID ADA06792 standard; protein; 373 AA.

DE Human secreted/transmembrane PRO polypeptide #140.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;  
RESULT 116  
ID ABJ72122 standard; protein; 373 AA.  
DE Human membrane bound receptor/protein PRO363 amino acid sequence.  
PN US2003065147-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;  
RESULT 117  
ID ADA39485 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein PRO363.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;  
RESULT 118  
ID ADA67009 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003068793-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;  
RESULT 119  
ID ADB22870 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003077111-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;  
RESULT 120  
ID ADB23643 standard; protein; 373 AA.  
DE Human PRO polypeptide SEQ ID NO 388.  
PN US2003077712-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;  
RESULT 121  
ID ADA92365 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003082712-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;  
RESULT 122  
ID ADB15428 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003087352-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;  
RESULT 123  
ID ADB83620 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003073814-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;  
RESULT 124  
ID ADB80726 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003088068-A1.  
PD 08-MAY-2003.

Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 134  
ID ADB39513 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003082764-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 135  
ID ADB78103 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003092886-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 136  
ID ADB73565 standard; protein; 373 AA.  
DE Human PRO polypeptide #8.  
PN US2003045462-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 137  
ID ADB87169 standard; protein; 373 AA.  
DE Human PRO polypeptide #65.  
PN US2003088067-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 138  
ID ADB84751 standard; protein; 373 AA.  
DE Human PRO polypeptide #85.  
PN US2003092890-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 139  
ID ADB47136 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003082687-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 140  
ID ADB83866 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003069397-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 141  
ID ADB86743 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003082697-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 142  
ID ADB73021 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003092887-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;



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RESULT 143
ID ADB76281 standard; protein; 373 AA.
DE Human PRO polypeptide #8.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 144
ID ADB77348 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 145
ID ADB34505 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 146
ID ADB35609 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 147
ID ADB33953 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 148
ID ADB35057 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 149
ID ADB36161 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 150
ID ADB46556 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 151
ID ADB43707 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 152
ID ADC57983 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 153
ID ADC55347 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 154
ID ADC12214 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 155
ID ADC61467 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 156
ID ADC63431 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 157
ID ADC66531 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 158
ID ADC56636 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003084375-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 159
ID ADC68655 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003084407-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 160
ID ADC62715 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1908; DB 7; Length 373;
RESULT 161
ID ADC67780 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.

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Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 162  
ID ADC11681 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein PRO363.  
PN US2003069403-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 163  
ID ADC41100 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein, PRO363.  
PN US2003072745-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 164  
ID ADC67155 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein, PRO363.  
PN US2003073131-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 165  
ID ADC62091 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein, PRO363.  
PN US2003073624-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 166  
ID ADC36859 standard; protein; 373 AA.  
DE Human PRO polypeptide #65.  
PN US2003088065-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 167  
ID ADC41724 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein, PRO363.  
PN US2003104998-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 168  
ID ADC21849 standard; protein; 373 AA.  
DE Human PRO polypeptide #65.  
PN US2003096969-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 169  
ID ADC50429 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003092106-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 170  
ID ADC71976 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003092107-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 171  
ID ADC59955 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003092105-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 172  
ID ADC49880 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003088064-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 173  
ID ADC49079 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003088070-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 174  
ID ADC49596 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003088071-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 175  
ID ADC47457 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003088072-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 176  
ID ADC52962 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein Seq ID388.  
PN US2003087365-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 177  
ID ADC57316 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein Seq ID388.  
PN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 178  
ID ADC60507 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 179  
ID ADC50982 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003087361-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 180



Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 199  
ID ADD06312 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003073816-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 200  
ID ADC80573 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003092103-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 201  
ID ADD11080 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003194774-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 202  
ID ADD10353 standard; protein; 373 AA.  
DE Human secreted/transmembrane PRO polypeptide #32.  
PN US2003105011-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 203  
ID ADC47961 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003194771-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 204  
ID ADD08873 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003073090-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 205  
ID ADC77831 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003088066-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 206  
ID ADC80021 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003087358-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 207  
ID ADD07122 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2002193300-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 208  
ID ADD55476 standard; protein; 373 AA.  
DE Human PRO polypeptide #140.

ID ADD11313 standard; protein; 373 AA.  
DE Human secreted/transmembrane PRO polypeptide #32.  
PN US2003105013-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 209  
ID ADD09490 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003194775-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 210  
ID ADC83369 standard; protein; 373 AA.  
DE Human PRO polypeptide #140.  
PN US2003059783-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 211  
ID ADD50794 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003105291-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 212  
ID ADD41203 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003203438-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 213  
ID ADD52342 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003194769-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 214  
ID ADD51040 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003105290-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 215  
ID ADD53082 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003194792-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 216  
ID ADD53634 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003203437-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 217  
ID ADD55476 standard; protein; 373 AA.  
DE Human PRO polypeptide #140.

PN US2003077593-A1.  
PD 24-APR-2003.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 218  
ID ADD37106 standard; protein; 373 AA.  
DE Human secreted/transmembrane PRO polypeptide #32.  
PN US2003105012-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 219  
ID ADD56434 standard; protein; 373 AA.  
DE Human PRO polypeptide #140.  
PN US2003077594-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 220  
ID ADD51790 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003194779-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 221  
ID ADD02589 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003203431-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 222  
ID ADD05021 standard; protein; 373 AA.  
DE Human PRO polypeptide #65.  
PN US2003096971-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 223  
ID ADD02023 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003203430-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 224  
ID ADD54205 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003203432-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 225  
ID ADD54872 standard; protein; 373 AA.  
DE Human PRO polypeptide #140.  
PN US2002132253-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 226  
ID ADD50275 standard; protein; 373 AA.  
DE Human PRO polypeptide #65.  
PN US2003096970-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 227  
ID ADD51286 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003105289-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 228  
ID ADE49093 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein, PRO363.  
PN US2003096744-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 229  
ID ADD92522 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US200319030-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 230  
ID ADD91418 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003199055-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 231  
ID ADE04032 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003199057-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 232  
ID ADE31891 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein PRO363.  
PN US2003068647-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 233  
ID ADE27026 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003087304-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 234  
ID ADE32329 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003194765-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 235  
ID ADE22261 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003199056-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 236

ID ADD79485 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003203428-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 237  
ID ADE35147 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein, PRO363.  
PN US2003203434-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 238  
ID ADE16261 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein, PRO363.  
PN US2003203435-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 239  
ID ADD72876 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein, PRO363.  
PN US2003203436-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 240  
ID ADE42021 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003194772-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 241  
ID ADE17838 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003199023-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 242  
ID ADD91970 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003199053-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 243  
ID ADE33433 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003194767-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 244  
ID ADE33985 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003194791-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 245  
ID ADD80037 standard; protein; 373 AA.

DE Human PRO polypeptide #194.  
PN US2003207417-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 246  
ID ADD93074 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003194768-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 247  
ID ADD72234 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein, PRO363.  
PN US2003194781-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 248  
ID ADE19494 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003199025-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 249  
ID ADE18942 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003199026-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 250  
ID ADE43138 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003199033-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 251  
ID ADD95927 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003199059-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 252  
ID ADE22813 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003199064-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 253  
ID ADD78931 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003203429-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 254  
ID ADE26493 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.

PN US2003087305-A1.  
 PD 08-MAY-2003.  
 Query Match 100.0%; Score 1908; DB 7; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 255  
 ID ADE32881 standard; protein; 373 AA.  
 DE Novel human secreted and transmembrane protein PRO363.  
 PN US2003194766-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 7; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 256  
 ID ADE42573 standard; protein; 373 AA.  
 DE Human PRO polypeptide #194.  
 PN US2003199032-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 7; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 257  
 ID ADE16885 standard; protein; 373 AA.  
 DE Human secreted/transmembrane protein, PRO363.  
 PN US2003203433-A1.  
 PD 30-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 7; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 258  
 ID ADD80589 standard; protein; 373 AA.  
 DE Human PRO polypeptide #194.  
 PN US2003207418-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 7; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 259  
 ID ADD89617 standard; protein; 373 AA.  
 DE Human PRO polypeptide #194.  
 PN US2003199028-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 7; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 260  
 ID ADE40901 standard; protein; 373 AA.  
 DE Human PRO polypeptide #194.  
 PN US2003199031-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 7; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 261  
 ID ADE04700 standard; protein; 373 AA.  
 DE Human PRO polypeptide #194.  
 PN US2003199034-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 7; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 262  
 ID ADE92829 standard; protein; 373 AA.  
 DE Human PRO polypeptide #194.  
 PN US2003194777-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 7; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 263  
 ID ADF46899 standard; protein; 373 AA.  
 DE Human secreted/transmembrane protein, PRO363.  
 PN US2003195333-A1.  
 PD 16-OCT-2003.

PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 7; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 264  
 ID ADF67430 standard; protein; 373 AA.  
 DE Human PRO363 amino acid sequence SEQ ID NO:503.  
 PN US2002198148-A1.  
 PD 26-DEC-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 7; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 265  
 ID ADG21538 standard; protein; 373 AA.  
 DE Novel human secreted and transmembrane protein PRO363.  
 PN US2003207355-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 7; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 266  
 ID ADG23179 standard; protein; 373 AA.  
 DE Novel human secreted and transmembrane protein PRO363.  
 PN US2003207384-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 7; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 267  
 ID ADF97514 standard; protein; 373 AA.  
 DE Human PRO polypeptide #194.  
 PN US2003207370-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 7; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 268  
 ID ADG80578 standard; protein; 373 AA.  
 DE Human PRO polypeptide #194.  
 PN US2003207373-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 7; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 269  
 ID ADG52656 standard; protein; 373 AA.  
 DE Human secreted/transmembrane protein, PRO363.  
 PN US2003216561-A1.  
 PD 20-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 7; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 270  
 ID ADG59976 standard; protein; 373 AA.  
 DE Human secreted/transmembrane protein, PRO363.  
 PN US2003206915-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 7; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 271  
 ID ADG80026 standard; protein; 373 AA.  
 DE Human PRO polypeptide #194.  
 PN US2003207372-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 7; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 272  
 ID ADH55318 standard; protein; 373 AA.  
 DE Novel human secreted and transmembrane protein PRO363.  
 PN US2003207381-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 273  
ID ADH5870 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207379-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 274  
ID ADI35684 standard; protein; 373 AA.  
DE Human PRO polypeptide #140.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 275  
ID ADI60736 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein, PRO363.  
PN US2003077700-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 276  
ID ADI64089 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207385-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 277  
ID ADI65038 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207386-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 278  
ID ADI63537 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207387-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 279  
ID ADH81951 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207388-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 280  
ID ADI00177 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 281  
ID ADH81399 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207377-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 282

ID ADM82568 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003087355-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 283  
ID ADN15967 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003087353-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 284  
ID ADN16596 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003087385-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 285  
ID ADN15415 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003087356-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 286  
ID ADN14863 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003087357-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 7; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 287  
ID ADC48833 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003092888-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 288  
ID ADC81125 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003092115-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 289  
ID ADE21004 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003100735-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 290  
ID ADE05848 standard; protein; 373 AA.  
DE Human PRO polypeptide #65.  
PN US2003100728-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 291  
ID ADD76573 standard; protein; 373 AA.



DE Human PRO polypeptide #194.  
PN US2003100087-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 292  
ID ADD75077 standard; protein; 373 AA.  
DE Human PRO polypeptide #65.  
PN US2003100712-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 293  
ID ADD75823 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003100717-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 294  
ID ADD85055 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003100722-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 295  
ID ADD86881 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003100738-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 296  
ID ADE20758 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003100734-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 297  
ID ADE39055 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003096362-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 298  
ID ADD87937 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003092113-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 299  
ID ADD86341 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003203440-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 300  
ID ADE05602 standard; protein; 373 AA.  
DE Human PRO polypeptide #65.  
PN US2003100733-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 301  
ID ADD73587 standard; protein; 373 AA.  
DE Human PRO polypeptide #65.  
PN US2003100711-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 302  
ID ADE75789 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003211571-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 303  
ID ADE48393 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein, PRO363.  
PN US2003104536-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 304  
ID ADD78427 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003100737-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 305  
ID ADE41314 standard; protein; 373 AA.  
DE Human secreted/transmembrane PRO polypeptide #32.  
PN US2003100497-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 306  
ID ADE23365 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003092108-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 307  
ID ADE21250 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003100736-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 308  
ID ADD77365 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003100732-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 309  
ID ADE20512 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003100733-A1.

PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 310  
ID ADD75577 standard; protein; 373 AA.  
DE Human PRO polypeptide #65.  
PN US2003100064-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 311  
ID ADD74093 standard; protein; 373 AA.  
DE Human PRO polypeptide #65.  
PN US2003100708-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 312  
ID ADD74339 standard; protein; 373 AA.  
DE Human PRO polypeptide #65.  
PN US2003100709-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 313  
ID ADD76069 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003100718-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 314  
ID ADD85561 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003100721-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 315  
ID ADE23917 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003092110-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 316  
ID ADE24560 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003092111-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 317  
ID ADD87385 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003203439-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 318  
ID ADE05110 standard; protein; 373 AA.  
DE Human PRO polypeptide #65.  
PN US2003100726-A1.  
PD 29-MAY-2003.  
PA (GAOW/) GAO W.  
PA (FONG/) FONG S.  
PA (FILV/) FILVAROFF E.  
PA (FERR/) FERRARA N.  
PA (EATO/) EATON D L.  
PA (DESN/) DESNOYERS L.  
PA (BOTS/) BOTSTEIN D.  
PA (BAKE/) BAKER K P.  
PA (ASHK/) ASHKENAZI A J.  
PD 10-JUL-2003.  
PN US2003130181-A1.  
ID ADE89494 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein, PRO363.  
PN US2003130181-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 320  
ID ADD76867 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003100715-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 321  
ID ADD86635 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003100719-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 322  
ID ADE89251 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003199062-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 323  
ID ADD78103 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003100731-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 324  
ID ADE18390 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003194794-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 325  
ID ADE88699 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003199054-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 326  
ID ADE89494 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein, PRO363.  
PN US2003130181-A1.  
PD 10-JUL-2003.  
PA (ASHK/) ASHKENAZI A J.  
PA (BAKE/) BAKER K P.  
PA (BOTS/) BOTSTEIN D.  
PA (DESN/) DESNOYERS L.  
PA (EATO/) EATON D L.  
PA (FERR/) FERRARA N.  
PA (FILV/) FILVAROFF E.  
PA (FONG/) FONG S.  
PA (GAOW/) GAO W.

PA (GERB/) GERBER H.  
 PA (GERE/) GERRITSEN M E.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GIRM/) GIRMALDI J C.  
 PA (GURN/) GURNEY A L.  
 PA (HILL/) HILLMAN K J.  
 PA (KLJA/) KIJAVIN I J.  
 PA (KUOS/) KUO S S.  
 PA (NAPI/) NAPIER M A.  
 PA (PANJ/) PAN J.  
 PA (PAON/) PAONI N F.  
 PA (ROYM/) ROY M A.  
 PA (SHEL/) SHELTON D L.  
 PA (STEW/) STEWART T A.  
 PA (TUMA/) TUMAS D.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 Query Match 100.0%; Score 1908; DB 8; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 327  
 ID ADD77611 standard; protein; 373 AA.  
 DE Novel human secreted and transmembrane protein PRO363.  
 PN US2003100729-A1.  
 PD 29-MAY-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 8; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 328  
 ID ADD77857 standard; protein; 373 AA.  
 DE Novel human secreted and transmembrane protein PRO363.  
 PN US2003100730-A1.  
 PD 29-MAY-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 8; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 329  
 ID ADD85315 standard; protein; 373 AA.  
 DE Novel human secreted and transmembrane protein PRO363.  
 PN US2003100725-A1.  
 PD 29-MAY-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 8; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 330  
 ID ADD73847 standard; protein; 373 AA.  
 DE Human PRO polypeptide #65.  
 PN US2003100710-A1.  
 PD 29-MAY-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 8; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 331  
 ID ADD74585 standard; protein; 373 AA.  
 DE Human PRO polypeptide #65.  
 PN US2003100713-A1.  
 PD 29-MAY-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 8; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 332  
 ID ADD77113 standard; protein; 373 AA.  
 DE Novel human secreted and transmembrane protein PRO363.  
 PN US2003100716-A1.  
 PD 29-MAY-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 8; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 333  
 ID ADD85807 standard; protein; 373 AA.  
 DE Novel human secreted and transmembrane protein PRO363.  
 PN US2003100720-A1.  
 PD 29-MAY-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 8; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 334  
 ID ADE05356 standard; protein; 373 AA.  
 DE Human PRO polypeptide #65.  
 PN US2003100723-A1.  
 PD 29-MAY-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 8; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 335  
 ID ADD74831 standard; protein; 373 AA.  
 DE Human PRO polypeptide #65.  
 PN US2003100724-A1.  
 PD 29-MAY-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 8; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 336  
 ID ADF61134 standard; protein; 373 AA.  
 DE Human secreted/transmembrane protein, PRO363.  
 PN US2003195345-A1.  
 PD 16-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 8; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 337  
 ID ADF39826 standard; protein; 373 AA.  
 DE Human secreted/transmembrane protein, PRO363.  
 PN US2003198994-A1.  
 PD 23-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 8; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 338  
 ID ADF45622 standard; protein; 373 AA.  
 DE Human secreted/transmembrane protein, PRO363.  
 PN US2003195148-A1.  
 PD 16-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 8; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 339  
 ID ADE94719 standard; protein; 373 AA.  
 DE Human PRO polypeptide #194.  
 PN US2003199027-A1.  
 PD 23-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 8; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 340  
 ID ADE91130 standard; protein; 373 AA.  
 DE Human PRO polypeptide #194.  
 PN US2003199061-A1.  
 PD 23-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 8; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 341  
 ID ADF35629 standard; protein; 373 AA.  
 DE Human PRO363 polypeptide.  
 PN US2003194760-A1.  
 PD 16-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 8; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 342  
 ID ADE95271 standard; protein; 373 AA.  
 DE Human PRO polypeptide #194.  
 PN US2003199052-A1.  
 PD 23-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Query Match 100.0%; Score 1908; DB 8; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
 RESULT 343  
 ID ADD85807 standard; protein; 373 AA.  
 DE Novel human secreted and transmembrane protein PRO363.  
 PN US2003100720-A1.  
 PD 29-MAY-2003.

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Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 343
ID ADE93381 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 344
ID ADF24018 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 345
ID ADF40450 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 346
ID ADF23394 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 347
ID ADF33377 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 348
ID ADF34962 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 349
ID ADF26844 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 350
ID ADF27480 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 351
ID ADE92277 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 352
ID ADE90578 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 353
ID ADF41074 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 354
ID ADF32753 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 355
ID ADF25119 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 356
ID ADF28220 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 357
ID ADF34009 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 358
ID ADF46246 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 359
ID ADE91725 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 360
ID ADG11879 standard; protein; 373 AA.
DE Human PRO363 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1908; DB 8; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.7e-145;
RESULT 361
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ID ADG05643 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003096959-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 362  
ID ADG27197 standard; protein; 373 AA.  
DE Human PRO polypeptide #65.  
PN US2003096962-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 363  
ID ADG02304 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003207352-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 364  
ID ADG22090 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207360-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 365  
ID ADG20160 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003207376-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 366  
ID ADF98066 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003207422-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 367  
ID ADG24283 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207426-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 368  
ID ADF98637 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003208055-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 369  
ID ADG03468 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003207351-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 370  
ID ADF99189 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003207353-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 371  
ID ADG16774 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003207359-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 372  
ID ADG05233 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003207375-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 373  
ID ADG19500 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003207425-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 374  
ID ADG11260 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003096967-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 375  
ID ADG13337 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003207357-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 376  
ID ADG08394 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207424-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 377  
ID ADG15564 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003219885-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 378  
ID ADG12039 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003096963-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 379  
ID ADF96962 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.

PN US2003207371-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 380  
ID ADG06147 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003207374-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 381  
ID ADG21731 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207389-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 382  
ID ADG04020 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003207423-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 383  
ID ADG24921 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207427-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 384  
ID ADF94596 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003096964-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 385  
ID ADG07218 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207350-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 386  
ID ADG07770 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207356-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 387  
ID ADG06692 standard; protein; 373 AA.  
DE Human PRO polypeptide #65.  
PN US2003096966-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 388  
ID ADG55265 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003194778-A1.

PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 389  
ID ADG60929 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207390-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 390  
ID ADG62033 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207428-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 391  
ID ADG82234 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003207358-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 392  
ID ADG57473 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207362-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 393  
ID ADG56921 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207364-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 394  
ID ADG55817 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207365-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 395  
ID ADG58577 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207368-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 396  
ID ADG70943 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207420-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 397  
ID ADH39036 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003096965-A1.  
PD 22-MAY-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 398  
ID ADG58025 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207363-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 399  
ID ADG53609 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207415-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 400  
ID ADG71495 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207421-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 401  
ID ADG50232 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein, PRO363.  
PN US2003207803-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 402  
ID ADG81682 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003207805-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 403  
ID ADH19749 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein PRO363.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 404  
ID ADH30644 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003077723-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 405  
ID ADH12011 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207419-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 406  
ID ADG49608 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein, PRO363.  
PN US2003215905-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;

Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 407  
ID ADG51480 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein, PRO363.  
PN US2003215908-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 408  
ID ADG52433 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207414-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 409  
ID ADG54161 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207416-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 410  
ID ADG48984 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein, PRO363.  
PN US2003216305-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 411  
ID ADG81130 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003194793-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 412  
ID ADG56369 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207366-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 413  
ID ADH12635 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207378-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 414  
ID ADG48360 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein, PRO363.  
PN US2003216560-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 415  
ID ADH21242 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein PRO363.  
PN US2003224358-A1.  
PD 04-DEC-2003.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 416

ID ADG61481 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207429-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 417  
ID ADH20282 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein PRO363.  
PN US2003219856-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 418  
ID ADH28568 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003022331-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 419  
ID ADG54713 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207367-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 420  
ID ADG59753 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207369-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 421  
ID ADG59856 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein, PRO363.  
PN US2004005312-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 422  
ID ADH43497 standard; protein; 373 AA.  
DE Human PRO polypeptide #32.  
PN US2003224984-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 423  
ID ADG58800 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein, PRO363.  
PN US2004005657-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 424  
ID ADG34126 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2004006206-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 425  
ID ADG62256 standard; protein; 373 AA.

DE Human secreted/transmembrane protein, PRO363.  
PN US2004006219-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 426  
ID ADI81177 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003207361-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 427  
ID ADI33596 standard; protein; 373 AA.  
DE Human PRO polypeptide #65.  
PN US2003096960-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 428  
ID ADH69690 standard; protein; 373 AA.  
DE Human PRO polypeptide #65.  
PN US2004019183-A1.  
PD 29-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 429  
ID ADH25281 standard; protein; 373 AA.  
DE Human neurotrophin homologue related protein sequence SEQ ID NO:59.  
PN EPI386931-A1.  
PD 04-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 430  
ID ADG09920 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2004009548-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 431  
ID ADI15391 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207382-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 432  
ID ADG09268 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2004009547-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 433  
ID ADI14723 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207383-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 434  
ID ADI29851 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.



PN US2003096961-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 435  
ID ADL18318 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207349-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 436  
ID ADM27248 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2004044179-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 437  
ID ADJ63599 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2004039164-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 438  
ID ADJ77494 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2004038336-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 439  
ID ADK82842 standard; protein; 373 AA.  
DE Human PRO polypeptide #32.  
PN US2004043927-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 440  
ID ADK66606 standard; protein; 373 AA.  
DE Human PRO polypeptide #65.  
PN US2004044180-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 441  
ID ADJ65616 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2004038335-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 442  
ID ADM27752 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2004048333-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 443  
ID ADM17058 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein, PRO363.  
PN US2004048332-A1.

PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 444  
ID ADL06892 standard; protein; 373 AA.  
DE Human secreted/transmembrane protein, PRO363.  
PN US2004063921-A1.  
PD 01-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 445  
ID ADM42476 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2004058424-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 446  
ID ADN05373 standard; protein; 373 AA.  
DE Antipeptidic protein sequence #858.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 447  
ID ADM28338 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2004077064-A1.  
PD 22-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 448  
ID ADO36720 standard; protein; 373 AA.  
DE Human UKW polypeptide, SEQ ID NO:2.  
PN EP1416279-A1.  
PD 06-MAY-2004.  
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 449  
ID ADI95820 standard; protein; 373 AA.  
DE Human PRO polypeptide #194.  
PN US2003077659-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 450  
ID ADI96372 standard; protein; 373 AA.  
DE Novel human secreted and transmembrane protein PRO363.  
PN US2003207354-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1908; DB 8; Length 373;  
Best Local Similarity 100.0%; Pred. No. 3.7e-145;  
RESULT 451  
ID AAB48146 standard; protein; 373 AA.  
DE Human A236 variant 2 polypeptide.  
PN WO200069885-A2.  
PD 23-NOV-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 99.8%; Score 1905; DB 4; Length 373;  
Best Local Similarity 99.7%; Pred. No. 6.5e-145;  
RESULT 452  
ID AAB48147 standard; protein; 373 AA.  
DE Human A236 variant 3 polypeptide.  
PN WO200069885-A2.  
PD 23-NOV-2000.

PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 99.8%; Score 1905; DB 4; Length 373;  
Best Local Similarity 99.7%; Pred. No. 6.5e-145;  
RESULT 453  
ID AAB48145 standard; protein; 373 AA.  
DE Human A236 variant 1 polypeptide.  
PN WO200069885-A2.  
PD 23-NOV-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 99.8%; Score 1905; DB 4; Length 373;  
Best Local Similarity 99.7%; Pred. No. 6.5e-145;  
RESULT 454  
ID AAB48126 standard; protein; 373 AA.  
DE Mouse A236 polypeptide.  
PN WO200069885-A2.  
PD 23-NOV-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 92.4%; Score 1763.5; DB 4; Length 373;  
Best Local Similarity 92.7%; Pred. No. 1.7e-133;  
RESULT 455  
ID AAE26449 standard; protein; 373 AA.  
DE Mouse A236 protein.  
PN US2002055139-A1.  
PD 09-MAY-2002.  
PA (HOLT/) HOLTZMAN D A.  
PA (SHAR/) SHARP J D.  
PA (LEIB/) LEIBY K R.  
PA (BOSS/) BOSSONE S.  
PA (PANY/) PAN Y.  
PA (BARN/) BARNES T M.  
PA (FRAS/) FRASER C C.  
PA (WRIG/) WRIGHTON N.  
PA (MYER/) MYERS P S.  
PA (KING/) KINGSBURY G.  
Query Match 92.4%; Score 1763.5; DB 5; Length 373;  
Best Local Similarity 92.7%; Pred. No. 1.7e-133;  
RESULT 456  
ID AAB48149 standard; protein; 373 AA.  
DE Mouse A236 variant 2 polypeptide.  
PN WO200069885-A2.  
PD 23-NOV-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 92.3%; Score 1760.5; DB 4; Length 373;  
Best Local Similarity 92.5%; Pred. No. 2.9e-133;  
RESULT 457  
ID AAB48150 standard; protein; 373 AA.  
DE Mouse A236 variant 3 polypeptide.  
PN WO200069885-A2.  
PD 23-NOV-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 92.3%; Score 1760.5; DB 4; Length 373;  
Best Local Similarity 92.5%; Pred. No. 2.9e-133;  
RESULT 458  
ID AAB48148 standard; protein; 373 AA.  
DE Mouse A236 variant 1 polypeptide.  
PN WO200069885-A2.  
PD 23-NOV-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 92.3%; Score 1760.5; DB 4; Length 373;  
Best Local Similarity 92.5%; Pred. No. 2.9e-133;  
RESULT 459  
ID AAB95862 standard; protein; 373 AA.  
DE Murine adipocytes-derived protein.  
PN WO200166720-A1.  
PD 13-SEP-2001.  
PA (KITA/) KITAMURA T.  
PA (TSUR/) TSURUGA H.  
Query Match 92.2%; Score 1759.5; DB 4; Length 373;  
Best Local Similarity 92.5%; Pred. No. 3.5e-133;  
RESULT 460  
ID ABO00483 standard; protein; 141 AA.  
DE Novel human polypeptide #70.  
PN WO2003023013-A2.

PD 20-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 36.3%; Score 692; DB 6; Length 141;  
Best Local Similarity 100.0%; Pred. No. 1.1e-47;  
RESULT 461  
ID ABO00802 standard; protein; 139 AA.  
DE Polypeptide encoded by novel human contig #53.  
PN WO2003023013-A2.  
PD 20-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 35.1%; Score 670; DB 6; Length 139;  
Best Local Similarity 99.3%; Pred. No. 6.3e-46;  
RESULT 462  
ID ABB83928 standard; protein; 365 AA.  
DE PCAR SEO ID NO 4.  
PN US2002059654-A1.  
PD 16-MAY-2002.  
PA (BUHL/) BUHLER T.  
PA (GADI/) GADIENT R A.  
PA (KORN/) KORN R.  
PA (MOVV/) MOVVA R.  
Query Match 24.7%; Score 471; DB 5; Length 365;  
Best Local Similarity 32.6%; Pred. No. 2.6e-29;  
RESULT 463  
ID AAW69697 standard; protein; 365 AA.  
DE Human coxsackievirus and Ad2 and Ad5 receptor HCAR protein.  
PN WO9833819-A1.  
PD 06-AUG-1998.  
PA (UYNY) UNIV NEW YORK STATE.  
Query Match 24.4%; Score 465; DB 2; Length 365;  
Best Local Similarity 31.6%; Pred. No. 8e-29;  
RESULT 464  
ID AAW57212 standard; protein; 365 AA.  
DE Human coxsackievirus and adenovirus receptor.  
PN WO9811221-A2.  
PD 19-MAR-1998.  
PA (DAND) DANA FARBER CANCER INST INC.  
Query Match 24.4%; Score 465; DB 2; Length 365;  
Best Local Similarity 31.6%; Pred. No. 8e-29;  
RESULT 465  
ID AAB47270 standard; protein; 365 AA.  
DE Human CAR.  
PN US6245966-B1.  
PD 12-JUN-2001.  
PA (UYTE-) UNIV TECHNOLOGY CORP.  
Query Match 24.4%; Score 465; DB 4; Length 365;  
Best Local Similarity 31.6%; Pred. No. 8e-29;  
RESULT 466  
ID ABB08040 standard; protein; 365 AA.  
DE Human coxsackie-adenovirus receptor (CAR).  
PN WO200229072-A2.  
PD 11-APR-2002.  
PA (NOVS) NOVARTIS AG.  
Query Match 24.4%; Score 465; DB 5; Length 365;  
Best Local Similarity 31.6%; Pred. No. 8e-29;  
RESULT 467  
ID ABJ37063 standard; protein; 365 AA.  
DE Human breast cancer / ovarian cancer related protein #39.  
PN WO2003000012-A2.  
PD 03-JAN-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 24.4%; Score 465; DB 6; Length 365;  
Best Local Similarity 31.6%; Pred. No. 8e-29;  
RESULT 468  
ID ADB97544 standard; protein; 365 AA.  
DE Human CAR wild-type protein.  
PN WO2003070915-A2.  
PD 28-AUG-2003.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 24.4%; Score 465; DB 7; Length 365;  
Best Local Similarity 31.6%; Pred. No. 8e-29;  
RESULT 469

ID ADN95226 standard; protein; 365 AA.  
DE Human BEC/LSC-related protein sequence SeqID148.  
FN WO2003080640-A1.  
PD 02-OCT-2003.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN) LICENTIA LTD.  
Query Match 24.4%; Score 465; DB 7; Length 365;  
Best Local Similarity 31.6%; Pred. No. 8e-29;  
RESULT 470  
ID ABU12046 standard; protein; 505 AA.  
DE Human NOV4a CG59871-01 protein SEQ ID 12.  
FN WO200281625-A2.  
PD 17-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 24.4%; Score 465; DB 6; Length 505;  
Best Local Similarity 31.7%; Pred. No. 1.3e-28;  
RESULT 471  
ID ADR66297 standard; protein; 358 AA.  
DE Human prostatic carcinoma derived protein SEQ ID 151 #2.  
FN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ-) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Query Match 24.1%; Score 459; DB 8; Length 358;  
Best Local Similarity 31.8%; Pred. No. 2.4e-28;  
RESULT 472  
ID ADR66858 standard; protein; 358 AA.  
DE Human prostatic carcinoma derived DNA SEQ ID 151 #4.  
FN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ-) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Query Match 24.1%; Score 459; DB 8; Length 358;  
Best Local Similarity 31.8%; Pred. No. 2.4e-28;  
RESULT 473  
ID AAB48123 standard; peptide; 86 AA.  
DE Human A236 immunoglobulin domain.  
FN WO2000069885-A2.  
PD 23-NOV-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 23.9%; Score 456; DB 4; Length 86;  
Best Local Similarity 100.0%; Pred. No. 5.8e-29;  
RESULT 474  
ID AAW57213 standard; protein; 376 AA.  
DE Mouse coxsackievirus and adenovirus receptor.  
FN WO9811221-A2.  
PD 19-MAR-1998.  
PA (DAND) DANA FARBER CANCER INST INC.  
Query Match 23.8%; Score 453.5; DB 2; Length 376;  
Best Local Similarity 32.0%; Pred. No. 7.1e-28;  
RESULT 475  
ID AAY72878 standard; protein; 352 AA.  
DE Human PRO5723 protein encoded by DNA82361 cDNA clone.  
FN WO200116319-A2.  
PD 08-MAR-2001.  
PA (GETH) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 4; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 476  
ID AAB50930 standard; protein; 352 AA.  
DE Human PRO5723 protein.  
FN WO200073452-A2.  
PD 07-DEC-2000.  
PA (GETH) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 4; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 477  
ID AAB5294 standard; protein; 352 AA.  
DE Human PRO5723 protein sequence SEQ ID NO:505.  
FN WO200073454-A1.  
PD 07-DEC-2000.  
PA (GETH) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 4; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 478  
ID ABB4956 standard; protein; 352 AA.  
DE Human PRO5723 protein sequence SEQ ID NO:280.  
FN WO20020690-A2.  
PD 03-JAN-2002.  
PA (GETH) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 5; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 479  
ID ABB95562 standard; protein; 352 AA.  
DE Human angiogenesis related protein PRO5723 SEQ ID NO: 280.  
FN WO200208284-A2.  
PD 31-JAN-2002.  
PA (GETH) GENENTECH INC.  
PA (BAKE/) BAKER K P.  
PA (FERR/) FERRARA N.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (MARS/) MARSTERS S A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (STEP/) STEPHAN J F.  
PA (WATA/) WATANABE C K.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 22.7%; Score 433; DB 5; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 480  
ID ABU58109 standard; protein; 352 AA.  
DE Human PRO polypeptide #141.  
FN US2003027163-A1.  
PD 06-FEB-2003.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 481  
ID ABU59187 standard; protein; 352 AA.  
DE Novel human secreted or transmembrane protein PRO5723.  
FN US2002132252-A1.  
PD 19-SEP-2002.  
PA (GETH) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 482  
ID ABU82699 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein PRO5723.  
FN US2003032023-A1.  
PD 13-FEB-2003.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 483  
ID ABU60618 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, #177.  
FN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 484  
ID ABU80846 standard; protein; 352 AA.  
DE Human PRO polypeptide #108.  
FN US2003036635-A1.  
PD 20-FEB-2003.

PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 485  
ID ABO33812 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003045687-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 486  
ID ABU14000 standard; protein; 352 AA.  
DE Human PRO5723 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 487  
ID ABU72585 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003003531-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 488  
ID ABG74762 standard; protein; 352 AA.  
DE Human PRO5723 protein.  
PN US2002192752-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 489  
ID ABU59334 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, #177.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 490  
ID ABO26031 standard; protein; 352 AA.  
DE Human PRO5723 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 491  
ID ABU82155 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003088063-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 492  
ID ABU59040 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, #177.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 493  
ID ABU92418 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 494  
ID ABU59483 standard; protein; 352 AA.  
DE Novel human secreted or transmembrane protein PRO3301.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 495  
ID ABU22249 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 496  
ID ABU10955 standard; protein; 352 AA.  
DE Human PRO polypeptide #141.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 497  
ID ABU81707 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 498  
ID ABU88646 standard; protein; 352 AA.  
DE Human secreted and transmembrane polypeptide PRO5723.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 499  
ID ABO34160 standard; protein; 352 AA.  
DE Human PRO5723 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 500  
ID ABJ72335 standard; protein; 352 AA.  
DE Human PRO5723 protein.  
PN US2003050448-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 501  
ID ADA38016 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein PRO5723.  
PN US2003008297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 502  
ID ADA21702 standard; protein; 352 AA.  
DE Human secreted/transmembrane polypeptide PRO5723.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 503  
ID ADA10489 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO5723.  
PN US2003059831-A1.  
PD 27-MAR-2003.

Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 504  
ID ADA18033 standard; protein; 352 AA.  
DE Human PRO5723 polypeptide.  
PN US2003054987-A1.  
PD 20-MAR-2003.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 505  
ID ADA28141 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein PRO5723.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 506  
ID ADA94721 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein PRO5723.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 507  
ID ADA38946 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein PRO5723.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 508  
ID ABJ72463 standard; protein; 352 AA.  
DE Human PRO5723 protein.  
PN US2003027988-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 509  
ID ADA93067 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein PRO5723.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 510  
ID ABO34358 standard; protein; 352 AA.  
DE Human secreted/transmembrane polypeptide PRO 5723.  
PN US2003044934-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 6; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 511  
ID ABO53246 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein PRO5723.  
PN US2003044806-A1.  
PD 06-MAR-2003.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 512  
ID ADA22628 standard; protein; 352 AA.  
DE Human secreted/transmembrane polypeptide PRO5723.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 513  
ID ABO22616 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein PRO5723.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
Query Match 22.7%; Score 433; DB 7; Length 352;

Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 514  
ID ADA06794 standard; protein; 352 AA.  
DE Human secreted/transmembrane PRO polypeptide #141.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 515  
ID ABJ72165 standard; protein; 352 AA.  
DE Human membrane bound receptor/protein PRO5723 amino acid sequence.  
PN US2003065147-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 516  
ID ADA39487 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein PRO5723.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 517  
ID ADB83706 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003073814-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 518  
ID ADB80812 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003088068-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 519  
ID ADB73353 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003096968-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 520  
ID ADB96513 standard; protein; 352 AA.  
DE Human PRO polypeptide #141.  
PN US2003054403-A1.  
PD 20-MAR-2003.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 521  
ID ADB78435 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003092889-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 522  
ID ADB85083 standard; protein; 352 AA.  
DE Human PRO polypeptide #108.  
PN US2003073817-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 523  
ID ADB78189 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.

PN US2003092886-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 524  
ID ADB87255 standard; protein; 352 AA.  
DE Human PRO polypeptide #108.  
PN US2003088067-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 525  
ID ADB84837 standard; protein; 352 AA.  
DE Human PRO polypeptide #108.  
PN US2003092890-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 526  
ID ADB83952 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003069397-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 527  
ID ADB73107 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003092887-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 528  
ID ADC57985 standard; protein; 352 AA.  
DE Human PRO polypeptide #141.  
PN US2003027754-A1.  
PD 06-FEB-2003.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 529  
ID ADC55349 standard; protein; 352 AA.  
DE Human PRO polypeptide #141.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 530  
ID ADC12216 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein PRO5723.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 531  
ID ADC56638 standard; protein; 352 AA.  
DE Human PRO polypeptide #141.  
PN US2003064375-A1.  
PD 03-APR-2003.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 532  
ID ADC11683 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein PRO5723.  
PN US2003069403-A1.  
PD 10-APR-2003.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 533

ID ADC36945 standard; protein; 352 AA.  
DE Human PRO polypeptide #108.  
PN US2003088065-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 534  
ID ADC21935 standard; protein; 352 AA.  
DE Human PRO polypeptide #108.  
PN US2003096969-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 535  
ID ADC49966 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003088064-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 536  
ID ADC49165 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003088070-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 537  
ID ADC49682 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003088071-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 538  
ID ADC47543 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003088072-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 539  
ID ADC14805 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003082546-A1.  
PD 01-MAY-2003.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 540  
ID ADC47288 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003105288-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 541  
ID ADD08337 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003068623-A1.  
PD 10-APR-2003.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 542  
ID ADC82162 standard; protein; 352 AA.  
DE Human PRO polypeptide #141.  
PN US2003083461-A1.

PD 01-MAY-2003.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 543  
ID ADD07804 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2002193299-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 544  
ID ADC78163 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003096972-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 545  
ID ADC82695 standard; protein; 352 AA.  
DE Human PRO polypeptide #141.  
PN US2003059833-A1.  
PD 27-MAR-2003.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 546  
ID ADD06398 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003073816-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 547  
ID ADD10569 standard; protein; 352 AA.  
DE Human secreted/transmembrane PRO polypeptide #140.  
PN US2003105011-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 548  
ID ADD08875 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003073090-A1.  
PD 17-APR-2003.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 549  
ID ADC77917 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003088066-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 550  
ID ADD07124 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2002193300-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 551  
ID ADD11529 standard; protein; 352 AA.  
DE Human secreted/transmembrane PRO polypeptide #140.  
PN US2003105013-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;

RESULT 552  
ID ADC83371 standard; protein; 352 AA.  
DE Human PRO polypeptide #141.  
PN US2003059783-A1.  
PD 27-MAR-2003.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 553  
ID ADD50880 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003105291-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 554  
ID ADD15380 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003059437-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 555  
ID ADD51126 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003105290-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 556  
ID ADD55478 standard; protein; 352 AA.  
DE Human PRO polypeptide #141.  
PN US2003077593-A1.  
PD 24-APR-2003.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 557  
ID ADD37322 standard; protein; 352 AA.  
DE Human secreted/transmembrane PRO polypeptide #140.  
PN US2003105012-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 558  
ID ADD56436 standard; protein; 352 AA.  
DE Human PRO polypeptide #141.  
PN US2003077594-A1.  
PD 24-APR-2003.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 559  
ID ADD50607 standard; protein; 352 AA.  
DE Human PRO polypeptide #108.  
PN US2003096971-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 560  
ID ADD54874 standard; protein; 352 AA.  
DE Human PRO polypeptide #141.  
PN US2002132253-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 561  
ID ADD50361 standard; protein; 352 AA.  
DE Human PRO polypeptide #108.  
PN US2003096970-A1.

PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 562  
ID ADD51372 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003105289-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 563  
ID ADE31893 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein PRO5723.  
PN US2003068647-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 564  
ID ADE27028 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003087304-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 565  
ID ADE26495 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003087305-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 566  
ID ADF67432 standard; protein; 352 AA.  
DE Human PRO5723 amino acid sequence SEQ ID NO:505.  
PN US2002198148-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 567  
ID ADE94085 standard; protein; 352 AA.  
DE Immune disease treatment/diagnosis related PRO5723.  
PN US2003082199-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 568  
ID ADI35686 standard; protein; 352 AA.  
DE Human PRO polypeptide #141.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 569  
ID ADI00179 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 7; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 570  
ID ADC48919 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003092888-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 571  
ID ADE21090 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003100735-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 572  
ID ADE05934 standard; protein; 352 AA.  
DE Human PRO polypeptide #108.  
PN US2003100728-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 573  
ID ADD75163 standard; protein; 352 AA.  
DE Human PRO polypeptide #108.  
PN US2003100712-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 574  
ID ADD75909 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003100717-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 575  
ID ADD85141 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003100722-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 576  
ID ADD86967 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003100738-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 577  
ID ADE20844 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003100734-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 578  
ID ADE39141 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003096362-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 579  
ID ADE05688 standard; protein; 352 AA.  
DE Human PRO polypeptide #108.  
PN US2003100727-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 580  
ID ADD73673 standard; protein; 352 AA.  
DE Human PRO polypeptide #108.



PN US2003100711-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 581  
ID ADD78513 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003100737-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 582  
ID ADE41530 standard; protein; 352 AA.  
DE Human secreted/transmembrane PRO polypeptide #140.  
PN US2003100497-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 583  
ID ADE21336 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003100736-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 584  
ID ADD77451 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003100732-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 585  
ID ADE20598 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003100733-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 586  
ID ADD75663 standard; protein; 352 AA.  
DE Human PRO polypeptide #108.  
PN US2003100064-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 587  
ID ADD74179 standard; protein; 352 AA.  
DE Human PRO polypeptide #108.  
PN US2003100708-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 588  
ID ADD74425 standard; protein; 352 AA.  
DE Human PRO polypeptide #108.  
PN US2003100709-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 589  
ID ADD76155 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003100718-A1.

PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 590  
ID ADD85647 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003100721-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 591  
ID ADE05196 standard; protein; 352 AA.  
DE Human PRO polypeptide #108.  
PN US2003100726-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 592  
ID ADD75409 standard; protein; 352 AA.  
DE Human PRO polypeptide #108.  
PN US2003100714-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 593  
ID ADD76953 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003100715-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 594  
ID ADD86721 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003100719-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 595  
ID ADD78189 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003100731-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 596  
ID ADD77697 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003100729-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 597  
ID ADD77943 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003100730-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 598  
ID ADD85401 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003100725-A1.  
PD 29-MAY-2003.

PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 599  
ID ADD73933 standard; protein; 352 AA.  
DE Human PRO polypeptide #108.  
PN US2003100710-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 600  
ID ADD74671 standard; protein; 352 AA.  
DE Human PRO polypeptide #108.  
PN US2003100713-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 601  
ID ADD77199 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003100716-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 602  
ID ADD85893 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003100720-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 603  
ID ADE05442 standard; protein; 352 AA.  
DE Human PRO polypeptide #108.  
PN US2003100723-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 604  
ID ADD74917 standard; protein; 352 AA.  
DE Human PRO polypeptide #108.  
PN US2003100724-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 605  
ID ADF35631 standard; protein; 352 AA.  
DE Human PRO5723 polypeptide.  
PN US2003194760-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 606  
ID ADG11881 standard; protein; 352 AA.  
DE Human PRO5723 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 607  
ID ADG05729 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003096959-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 608  
ID ADG27283 standard; protein; 352 AA.  
DE Human PRO polypeptide #108.  
PN US2003096962-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 609  
ID ADG11346 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003096967-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 610  
ID ADG12125 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003096963-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 611  
ID ADF94682 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003096964-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 612  
ID ADG06778 standard; protein; 352 AA.  
DE Human PRO polypeptide #108.  
PN US2003096966-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 613  
ID ADH39122 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003096965-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 614  
ID ADH19751 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein PRO5723.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 615  
ID ADH21244 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein PRO5723.  
PN US2003224358-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 616  
ID ADH20284 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein PRO5723.  
PN US2003219856-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 617

ID ADH43713 standard; protein; 352 AA.  
DE Human PRO polypeptide #140.  
PN US2003224984-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 618  
ID ADG34212 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2004006206-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 619  
ID ADI33682 standard; protein; 352 AA.  
DE Human PRO polypeptide #108.  
PN US2003096960-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 620  
ID ADH69776 standard; protein; 352 AA.  
DE Human PRO polypeptide #108.  
PN US2004019183-A1.  
PD 29-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 621  
ID ADI29937 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2003096961-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 622  
ID ADM27334 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO5723.  
PN US2004044179-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 623  
ID ADK83058 standard; protein; 352 AA.  
DE Human PRO polypeptide #140.  
PN US2004043927-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 624  
ID ADK66692 standard; protein; 352 AA.  
DE Human PRO polypeptide #108.  
PN US2004044180-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 22.7%; Score 433; DB 8; Length 352;  
Best Local Similarity 33.8%; Pred. No. 2.9e-26;  
RESULT 625  
ID ARU12047 standard; protein; 422 AA.  
DE Human NOV5a CG59883-01 protein SEQ ID 14.  
PN WO200281625-A2.  
PD 17-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 22.2%; Score 424.5; DB 6; Length 422;  
Best Local Similarity 29.9%; Pred. No. 1.8e-25;  
RESULT 626  
ID AAW69698 standard; protein; 352 AA.  
DE Mouse coxsackievirus and Ad2 and Ad5 receptor MCAR protein.  
PN WO9833819-A1.  
PD 06-AUG-1998.  
PA (UYNY ) UNIV NEW YORK STATE.  
Query Match 22.1%; Score 422.5; DB 2; Length 352;  
Best Local Similarity 29.7%; Pred. No. 2e-25;  
RESULT 627  
ID ABB83927 standard; protein; 261 AA.  
DE C-terminally truncated pCAR SEQ ID NO 2.  
PN US2002059654-A1.  
PD 16-MAY-2002.  
PA (BUHL/) BUHLER T.  
PA (GADI/) GADIANT R A.  
PA (KORN/) KORN R.  
PA (MOVV/) MOVVA R.  
Query Match 19.8%; Score 378.5; DB 5; Length 261;  
Best Local Similarity 34.6%; Pred. No. 4.8e-22;  
RESULT 628  
ID ADL67136 standard; protein; 430 AA.  
DE Human B7-H5 protein SEQ ID NO:6.  
PN WO2004022594-A2.  
PD 18-MAR-2004.  
PA (CVTO-) CYTOS BIOTECHNOLOGY AG.  
Query Match 19.0%; Score 362.5; DB 8; Length 430;  
Best Local Similarity 29.5%; Pred. No. 1.8e-20;  
RESULT 629  
ID ABU08259 standard; protein; 431 AA.  
DE Human voltage-gated sodium channel beta subunit HIPHUM30.  
PN GB2376235-A.  
PD 11-DEC-2002.  
PA (GLAX ) GLAXO GROUP LTD.  
Query Match 18.9%; Score 361; DB 6; Length 431;  
Best Local Similarity 30.2%; Pred. No. 2.4e-20;  
RESULT 630  
ID ABR82054 standard; protein; 431 AA.  
DE Human cell adhesion molecule BT-IgSF protein SEQ ID NO:2.  
PN EPI321475-A1.  
PD 25-JUN-2003.  
PA (MORG ) MORINAGA MILK IND CO LTD.  
Query Match 18.9%; Score 361; DB 6; Length 431;  
Best Local Similarity 30.2%; Pred. No. 2.4e-20;  
RESULT 631  
ID ABB10359 standard; protein; 426 AA.  
DE Human cDNA SEQ ID NO: 667.  
PN WO200154474-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 18.9%; Score 360; DB 4; Length 426;  
Best Local Similarity 30.2%; Pred. No. 2.9e-20;  
RESULT 632  
ID ABP66946 standard; protein; 426 AA.  
DE Human polypeptide SEQ ID NO 667.  
PN US2002090672-A1.  
PD 11-JUL-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 18.9%; Score 360; DB 5; Length 426;  
Best Local Similarity 30.2%; Pred. No. 2.9e-20;  
RESULT 633  
ID ADC42862 standard; protein; 431 AA.  
DE REMAP protein #22.  
PN WO2003027228-A2.  
PD 03-APR-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 18.9%; Score 360; DB 7; Length 431;  
Best Local Similarity 30.2%; Pred. No. 2.9e-20;  
RESULT 634  
ID ADI00601 standard; protein; 431 AA.  
DE Human coxsackie and adenovirus receptor like 1 (CXADR11) protein.  
PN WO2003104275-A2.  
PD 18-DEC-2003.  
PA (ONCO-) ONCOTHERAPY SCI INC.

PA (UYTY ) UNIV TOKYO.  
Query Match 18.9%; Score 360; DB 8; Length 431;  
Best Local Similarity 30.2%; Pred. No. 2.9e-20;  
RESULT 635  
ID AAU83699 standard; protein; 290 AA.  
DE Human PRO protein, Seq ID No 216.  
PN WO200208288-A2.  
PD 31-JAN-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 18.7%; Score 357; DB 5; Length 290;  
Best Local Similarity 31.5%; Pred. No. 3e-20;  
RESULT 636  
ID ADL67140 standard; protein; 428 AA.  
DE Mouse B7-H5 protein SEQ ID No:10.  
PN WO2004022594-A2.  
PD 18-MAR-2004.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Query Match 18.5%; Score 352.5; DB 8; Length 428;  
Best Local Similarity 29.4%; Pred. No. 1.2e-19;  
RESULT 637  
ID ADP29332 standard; protein; 330 AA.  
DE Human secreted protein SEQ ID #99.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 18.4%; Score 350.5; DB 8; Length 330;  
Best Local Similarity 27.3%; Pred. No. 1.2e-19;  
RESULT 638  
ID AAW82731 standard; protein; 397 AA.  
DE Adenovirus PACSG2SCAR.sig chimeric protein.  
PN WO9854346-A1.  
PD 03-DEC-1998.  
PA (GENV-) GENVEC INC.  
Query Match 18.4%; Score 350.5; DB 2; Length 397;  
Best Local Similarity 28.2%; Pred. No. 1.5e-19;  
RESULT 639  
ID AAB48124 standard; peptide; 65 AA.  
DE Human A236 immunoglobulin domain.  
PN WO200069885-A2.  
PD 23-NOV-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 18.3%; Score 350; DB 4; Length 65;  
Best Local Similarity 100.0%; Pred. No. 1.4e-20;  
RESULT 640  
ID AAW82729 standard; protein; 264 AA.  
DE Adenovirus PACTSG2-SCAR protein.  
PN WO9854346-A1.  
PD 03-DEC-1998.  
PA (GENV-) GENVEC INC.  
Query Match 18.0%; Score 342.5; DB 2; Length 264;  
Best Local Similarity 33.3%; Pred. No. 3.9e-19;  
RESULT 641  
ID AAW82730 standard; protein; 277 AA.  
DE Adenovirus SCAR.RGD protein.  
PN WO9854346-A1.  
PD 03-DEC-1998.  
PA (GENV-) GENVEC INC.  
Query Match 17.9%; Score 341; DB 2; Length 277;  
Best Local Similarity 34.6%; Pred. No. 5.5e-19;  
RESULT 642  
ID ADA50170 standard; protein; 412 AA.  
DE Human CAR/SCF fusion protein.  
PN US2003092068-A1.  
PD 15-MAY-2003.  
PA (ITOH/) ITOH A.  
PA (HANA/) HANAZONO Y.  
PA (OKAD/) OKADA T.  
PA (OZAW/) OZAWA K.  
Query Match 17.9%; Score 341; DB 6; Length 412;  
Best Local Similarity 34.6%; Pred. No. 9.4e-19;  
RESULT 644  
ID ADA50172 standard; protein; 493 AA.  
DE Human CAR/mouse anti-CD34 antibody fusion protein.  
PN US2003092068-A1.  
PD 15-MAY-2003.  
PA (ITOH/) ITOH A.  
PA (HANA/) HANAZONO Y.  
PA (OKAD/) OKADA T.  
PA (OZAW/) OZAWA K.  
Query Match 17.9%; Score 341; DB 6; Length 412;  
Best Local Similarity 34.6%; Pred. No. 9.4e-19;  
RESULT 645  
ID ABU62399 standard; protein; 466 AA.  
DE Chimeric CAR/Hg/Pro-A gene product.  
PN US6524572-B1.  
PD 25-FEB-2003.  
PA (RAIN-) RAINBOW THERAPEUTIC CO.  
Query Match 17.8%; Score 340.5; DB 6; Length 466;  
Best Local Similarity 27.0%; Pred. No. 1.2e-18;  
RESULT 646  
ID ADA50158 standard; protein; 393 AA.  
DE Human CAR/mouse SCF mature fusion protein.  
PN US2003092068-A1.  
PD 15-MAY-2003.  
PA (ITOH/) ITOH A.  
PA (HANA/) HANAZONO Y.  
PA (OKAD/) OKADA T.  
PA (OZAW/) OZAWA K.  
Query Match 17.6%; Score 335; DB 6; Length 393;  
Best Local Similarity 35.4%; Pred. No. 2.7e-18;  
RESULT 647  
ID ADA50157 standard; protein; 393 AA.  
DE Human CAR/SCF mature fusion protein.  
PN US2003092068-A1.  
PD 15-MAY-2003.  
PA (ITOH/) ITOH A.  
PA (HANA/) HANAZONO Y.  
PA (OKAD/) OKADA T.  
PA (OZAW/) OZAWA K.  
Query Match 17.6%; Score 335; DB 6; Length 393;  
Best Local Similarity 35.4%; Pred. No. 2.7e-18;  
RESULT 648  
ID ADA50159 standard; protein; 474 AA.  
DE Human CAR/mouse anti-CD34 antibody mature fusion protein.  
PN US2003092068-A1.  
PD 15-MAY-2003.  
PA (ITOH/) ITOH A.  
PA (HANA/) HANAZONO Y.  
PA (OKAD/) OKADA T.  
PA (OZAW/) OZAWA K.  
Query Match 17.6%; Score 335; DB 6; Length 393;  
Best Local Similarity 35.4%; Pred. No. 2.7e-18;  
RESULT 649  
ID AAB65841 standard; protein; 365 AA.  
DE Murine mature INTERCEPT 258 SEQ ID NO: 40.  
PN WO200078808-A1.  
PD 28-DEC-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 16.8%; Score 321; DB 4; Length 365;  
Best Local Similarity 28.4%; Pred. No. 3.3e-17;  
RESULT 650  
ID AAB65840 standard; protein; 394 AA.  
DE Murine INTERCEPT 258 SEQ ID NO: 39.  
PN WO200078808-A1.  
PD 28-DEC-2000.

PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 16.8%; Score 321; DB 4; Length 394;  
Best Local Similarity 28.4%; Pred. No. 3.6e-17;  
RESULT 651  
ID AAB65908 standard; protein; 394 AA.  
DE Murine secreted protein related protein SEQ ID NO: 142.  
PN WO200078808-A1.  
PD 28-DEC-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 16.8%; Score 320; DB 4; Length 394;  
Best Local Similarity 28.4%; Pred. No. 4.4e-17;  
RESULT 652  
ID AAB65910 standard; protein; 394 AA.  
DE Murine secreted protein related protein SEQ ID NO: 146.  
PN WO200078808-A1.  
PD 28-DEC-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 16.8%; Score 320; DB 4; Length 394;  
Best Local Similarity 28.4%; Pred. No. 4.4e-17;  
RESULT 653  
ID AAB65911 standard; protein; 394 AA.  
DE Murine secreted protein related protein SEQ ID NO: 148.  
PN WO200078808-A1.  
PD 28-DEC-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 16.8%; Score 320; DB 4; Length 394;  
Best Local Similarity 28.4%; Pred. No. 4.4e-17;  
RESULT 654  
ID AAB65909 standard; protein; 394 AA.  
DE Murine secreted protein related protein SEQ ID NO: 144.  
PN WO200078808-A1.  
PD 28-DEC-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 16.6%; Score 317; DB 4; Length 394;  
Best Local Similarity 28.2%; Pred. No. 7.6e-17;  
RESULT 655  
ID ADF83097 standard; protein; 326 AA.  
DE Human corticol thymocyte receptor CTXL, overexpressed in cancer.  
PN WO200310000-A2.  
PD 04-DEC-2003.  
PA (TULA-) TULARIK INC.  
Query Match 16.5%; Score 315.5; DB 8; Length 326;  
Best Local Similarity 30.0%; Pred. No. 7.8e-17;  
RESULT 656  
ID AAB61480 standard; protein; 325 AA.  
DE Human CTH protein.  
PN WO200100672-A1.  
PD 04-JAN-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 16.5%; Score 314.5; DB 4; Length 325;  
Best Local Similarity 29.4%; Pred. No. 9.3e-17;  
RESULT 657  
ID AAY87251 standard; protein; 327 AA.  
DE Human signal peptide containing protein HSP-28 SEQ ID NO: 28.  
PN WO20000610-A2.  
PD 06-JAN-2000.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 16.2%; Score 309.5; DB 3; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 658  
ID AAY94857 standard; protein; 327 AA.  
DE Human protein clone HPI0568.  
PN WO200005367-A2.  
PD 03-FEB-2000.  
PA (SAGA) SAGAMI CHEM RES CENT.  
PA (PROT-) PROTEGENE INC.  
Query Match 16.2%; Score 309.5; DB 3; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 659  
ID AAY97585 standard; protein; 327 AA.  
DE Human secreted protein PRO7154.  
PN WO200075317-A2.  
PD 14-DEC-2000.

PA (GETH) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 4; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 660  
ID ABB90354 standard; protein; 327 AA.  
DE Human polypeptide SEQ ID NO 2730.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 16.2%; Score 309.5; DB 5; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 661  
ID AUB3709 standard; protein; 327 AA.  
DE Human PRO protein, Seq ID No 236.  
PN WO200208288-A2.  
PD 31-JAN-2002.  
PA (GETH) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 5; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 662  
ID AUB08056 standard; protein; 327 AA.  
DE Human PRO polypeptide #118.  
PN US200303653-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 6; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 663  
ID ABO33922 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003045687-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 6; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 664  
ID ABO82165 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003088063-A1.  
PD 08-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 6; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 665  
ID ABJ72345 standard; protein; 327 AA.  
DE Human PRO7154 protein.  
PN US2003050448-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 6; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 666  
ID ABJ72473 standard; protein; 327 AA.  
DE Human PRO7154 protein.  
PN US2003027988-A1.  
PD 06-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 6; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 667  
ID ABO34368 standard; protein; 327 AA.  
DE Human secreted/transmembrane polypeptide PRO 7154.  
PN US2003044934-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 6; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 668  
ID ABJ72175 standard; protein; 327 AA.  
DE Human membrane bound receptor/protein PRO7154 amino acid sequence.  
PN US2003065147-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.

Query Match 16.2%; Score 309.5; DB 7; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 669  
ID ADB83726 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003073814-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 7; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 670  
ID ADB80832 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003088068-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 7; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 671  
ID ADB73373 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003096968-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 7; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 672  
ID ADB78455 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003092889-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 7; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 673  
ID ADB85103 standard; protein; 327 AA.  
DE Human PRO polypeptide #118.  
PN US2003073817-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 7; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 674  
ID ADB78209 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003092886-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 7; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 675  
ID ADB87275 standard; protein; 327 AA.  
DE Human PRO polypeptide #118.  
PN US2003088067-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 7; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 676  
ID ADB84857 standard; protein; 327 AA.  
DE Human PRO polypeptide #118.  
PN US2003092890-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 7; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 677  
ID ADB83972 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003069397-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 7; Length 327;

Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 678  
ID ADB73127 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003092887-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 7; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 679  
ID ADC36965 standard; protein; 327 AA.  
DE Human PRO polypeptide #118.  
PN US2003088065-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 7; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 680  
ID ADC21955 standard; protein; 327 AA.  
DE Human PRO polypeptide #118.  
PN US2003096969-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 7; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 681  
ID ADC49986 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003088064-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 7; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 682  
ID ADC49185 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003088070-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 7; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 683  
ID ADC49702 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003088071-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 7; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 684  
ID ADC47563 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003088072-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 7; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 685  
ID ADC47308 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003105288-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 7; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 686  
ID ADC78183 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003096972-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 7; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 687  
ID ADB83972 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003069397-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 7; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;

RESULT 687  
ID ADE05954 standard; protein; 327 AA.  
DE Human PRO polypeptide #118.  
PN US2003100728-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 7; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 688  
ID ADC77937 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003088066-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 689  
ID ADD50900 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003105291-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 7; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 690  
ID ADD51146 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003105290-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 7; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 691  
ID ADD50627 standard; protein; 327 AA.  
DE Human PRO polypeptide #118.  
PN US2003096971-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 7; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 692  
ID ADD50381 standard; protein; 327 AA.  
DE Human PRO polypeptide #118.  
PN US2003096970-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 7; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 693  
ID ADD51392 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003105289-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 7; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 694  
ID ADC48939 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003052888-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 695  
ID ADE21110 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003100735-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 696  
ID ADE05954 standard; protein; 327 AA.  
DE Human PRO polypeptide #118.  
PN US2003100728-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 697  
ID ADD75183 standard; protein; 327 AA.  
DE Human PRO polypeptide #118.  
PN US2003100712-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 698  
ID ADD75929 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003100717-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 699  
ID ADD85161 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003100722-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 700  
ID ADD86987 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003100738-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 701  
ID ADE20864 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003100734-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 702  
ID ADE39161 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003096362-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 703  
ID ADE05708 standard; protein; 327 AA.  
DE Human PRO polypeptide #118.  
PN US2003100727-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 704  
ID ADD73693 standard; protein; 327 AA.  
DE Human PRO polypeptide #118.  
PN US2003100711-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 705  
ID ADD78533 standard; protein; 327 AA.

DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003100737-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 706  
ID ADE21356 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003100736-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 707  
ID ADD77471 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003100732-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 708  
ID ADE20618 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003100733-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 709  
ID ADD75683 standard; protein; 327 AA.  
DE Human PRO polypeptide #118.  
PN US2003100064-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 710  
ID ADD74445 standard; protein; 327 AA.  
DE Human PRO polypeptide #118.  
PN US2003100709-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 711  
ID ADD74445 standard; protein; 327 AA.  
DE Human PRO polypeptide #118.  
PN US2003100709-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 712  
ID ADD76175 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003100718-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 713  
ID ADD85667 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003100721-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 714  
ID ADE05216 standard; protein; 327 AA.  
DE Human PRO polypeptide #118.

PN US2003100726-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 715  
ID ADD75429 standard; protein; 327 AA.  
DE Human PRO polypeptide #118.  
PN US2003100714-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 716  
ID ADD76973 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003100715-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 717  
ID ADD86741 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003100719-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 718  
ID ADD78209 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003100731-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 719  
ID ADD77717 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003100729-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 720  
ID ADD77963 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003100730-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 721  
ID ADD85421 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003100725-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 722  
ID ADD73953 standard; protein; 327 AA.  
DE Human PRO polypeptide #118.  
PN US2003100710-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 723  
ID ADD74691 standard; protein; 327 AA.  
DE Human PRO polypeptide #118.  
PN US2003100713-A1.



PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 724  
ID ADG77219 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003100716-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 725  
ID ADH85913 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003100720-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 726  
ID ADE05462 standard; protein; 327 AA.  
DE Human PRO polypeptide #118.  
PN US2003100723-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 727  
ID ADD74937 standard; protein; 327 AA.  
DE Human PRO polypeptide #118.  
PN US2003100724-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 728  
ID ADG05749 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003096959-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 729  
ID ADG27303 standard; protein; 327 AA.  
DE Human PRO polypeptide #118.  
PN US2003096962-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 730  
ID ADG11366 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003096967-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 731  
ID ADG12145 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003096963-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 732  
ID ADP94702 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003096964-A1.  
PD 22-MAY-2003.

PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 733  
ID ADG06798 standard; protein; 327 AA.  
DE Human PRO polypeptide #118.  
PN US2003096966-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 734  
ID ADH39142 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003096965-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 735  
ID ADG34232 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2004006206-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 736  
ID ADI33702 standard; protein; 327 AA.  
DE Human PRO polypeptide #118.  
PN US2003096960-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 737  
ID ADH69796 standard; protein; 327 AA.  
DE Human PRO polypeptide #118.  
PN US2004019183-A1.  
PD 29-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 738  
ID ADI29957 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2003096961-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 739  
ID ADM27354 standard; protein; 327 AA.  
DE Novel human secreted and transmembrane protein PRO7154.  
PN US2004044179-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 740  
ID ADK66712 standard; protein; 327 AA.  
DE Human PRO polypeptide #118.  
PN US2004044180-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 309.5; DB 8; Length 327;  
Best Local Similarity 30.2%; Pred. No. 2.4e-16;  
RESULT 741  
ID AAB53307 standard; protein; 365 AA.  
DE Human colon cancer antigen protein sequence SEQ ID NO:847.  
PN WO200055351-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 16.2%; Score 309.5; DB 3; Length 365;  
Best Local Similarity 30.2%; Pred. No. 2.8e-16;  
RESULT 742  
ID AAG75613 standard; protein; 365 AA.  
DE Human colon cancer antigen protein SEQ ID NO:6377.  
PN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 16.2%; Score 309.5; DB 4; Length 365;  
Best Local Similarity 30.2%; Pred. No. 2.8e-16;  
RESULT 743  
ID AAW14146 standard; protein; 319 AA.  
DE Human A33 antigen.  
PN WO9708189-A1.  
PD 06-MAR-1997.  
PA (LUDW-) LUDWIG INST CANCER RES.  
Query Match 16.2%; Score 308.5; DB 2; Length 319;  
Best Local Similarity 31.2%; Pred. No. 2.8e-16;  
RESULT 744  
ID AAY23323 standard; protein; 319 AA.  
DE Amino acid sequence of the A33 antigen.  
PN WO9927098-A2.  
PD 03-JUN-1999.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 308.5; DB 2; Length 319;  
Best Local Similarity 31.2%; Pred. No. 2.8e-16;  
RESULT 745  
ID AAB65863 standard; protein; 319 AA.  
DE Human A33 protein SEQ ID NO: 67.  
PN WO200078808-A1.  
PD 28-DEC-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 16.2%; Score 308.5; DB 4; Length 319;  
Best Local Similarity 31.2%; Pred. No. 2.8e-16;  
RESULT 746  
ID ADA10947 standard; protein; 319 AA.  
DE Human cDNA differentially expressed in colon cancer #43 product.  
PN US2002160382-A1.  
PD 31-OCT-2002.  
PA (LASE-) LASEK A W.  
PA (JONE-) JONES D A.  
Query Match 16.2%; Score 308.5; DB 6; Length 319;  
Best Local Similarity 31.2%; Pred. No. 2.8e-16;  
RESULT 747  
ID ADH62533 standard; protein; 319 AA.  
DE Human A33 antigenic protein.  
PN US2003171568-A1.  
PD 11-SEP-2003.  
PA (ASHK-) ASHKENAZI A.  
PA (FONG-) FONG S.  
PA (GODD-) GODDARD A.  
PA (GURN-) GURNEY A L.  
PA (NAPI-) NAPIER M A.  
PA (TUMA-) TUMAS D.  
PA (WOOD-) WOOD W I.  
Query Match 16.2%; Score 308.5; DB 7; Length 319;  
Best Local Similarity 31.2%; Pred. No. 2.8e-16;  
RESULT 748  
ID ADN39847 standard; protein; 319 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C217.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (BOSB-) BOS BIOTECHNOLOGY INC.  
Query Match 16.2%; Score 308.5; DB 7; Length 319;  
Best Local Similarity 31.2%; Pred. No. 2.8e-16;  
RESULT 749  
ID ADN35289 standard; protein; 319 AA.  
DE Human A33 antigen protein.  
PN WO2004031105-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 308.5; DB 8; Length 319;  
Best Local Similarity 31.2%; Pred. No. 2.8e-16;

RESULT 750  
ID ADP54587 standard; protein; 319 AA.  
DE Human PRO protein sequence SEQ ID NO:563.  
PN WO2004039956-A2.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 16.2%; Score 308.5; DB 8; Length 319;  
Best Local Similarity 31.2%; Pred. No. 2.8e-16;  
RESULT 751  
ID ABP62881 standard; protein; 336 AA.  
DE Human polypeptide SEQ ID NO 318.  
PN WO200218424-A2.  
PD 07-MAR-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 16.2%; Score 308.5; DB 5; Length 336;  
Best Local Similarity 31.2%; Pred. No. 3e-16;  
RESULT 752  
ID ADK40854 standard; protein; 316 AA.  
DE Human A33 molecule.  
PN US6699688-B1.  
PD 02-MAR-2004.  
PA (UTNY ) UNIV NEW YORK STATE RES FOUND.  
Query Match 16.1%; Score 308; DB 8; Length 316;  
Best Local Similarity 31.1%; Pred. No. 3e-16;  
RESULT 753  
ID AAY95024 standard; protein; 325 AA.  
DE Human clone vc51.1 deletional variant ORF1, SEQ ID NO:124.  
PN WO200011015-A1.  
PD 02-MAR-2000.  
PA (ALPH-) ALPHAGENE INC.  
Query Match 16.1%; Score 308; DB 3; Length 325;  
Best Local Similarity 29.8%; Pred. No. 3.1e-16;  
RESULT 754  
ID AAY76303 standard; protein; 389 AA.  
DE Fragment of human secreted protein encoded by gene 29.  
PN WO9958660-A1.  
PD 18-NOV-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 16.1%; Score 307.5; DB 3; Length 389;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 755  
ID ADE11956 standard; protein; 389 AA.  
DE Human secreted polypeptide #210.  
PN US2003100051-A1.  
PD 29-MAY-2003.  
PA (RUBE-) RUBEN S M.  
PA (FLOR-) FLORENCE K A.  
PA (NIJU-) NI J.  
PA (ROSE-) ROSEN C A.  
PA (CART-) CARTER K C.  
PA (MOOR-) MOORE P A.  
PA (OLSE-) OLSEN H S.  
PA (SHIY-) SHI Y.  
PA (YOUN-) YOUNG P E.  
PA (WEIY-) WEI Y.  
PA (BREW-) BREWER L A.  
PA (SOPP-) SOPPET D R.  
PA (LAFLE-) LAFLEUR D W.  
PA (ENDR-) ENDRESS G A.  
PA (EBNE-) EBNER R.  
PA (BIRS-) BIRSE C E.  
Query Match 16.1%; Score 307.5; DB 7; Length 389;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 756  
ID AAY05286 standard; protein; 390 AA.  
DE EGF-like homologue PRO246.  
PN WO9914327-A2.  
PD 25-MAR-1999.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 2; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 757  
ID AAY13351 standard; protein; 390 AA.

DE Amino acid sequence of protein PRO246.  
PN WO9914328-A2.  
PD 25-MAR-1999.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 2; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 758  
ID AAY27096 standard; protein; 390 AA.  
DE Human viral receptor protein (ACVRP).  
PN US5942606-A.  
PD 24-AUG-1999.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 16.1%; Score 307.5; DB 2; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 759  
ID AAY94999 standard; protein; 390 AA.  
DE Human secreted protein vc51\_1, SEQ ID NO:38.  
PN WO200011015-A1.  
PD 02-MAR-2000.  
PA (ALPH-) ALPHAGEN INC.  
Query Match 16.1%; Score 307.5; DB 3; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 760  
ID AAY8574 standard; protein; 390 AA.  
DE Human PRO246 amino acid sequence.  
PN WO200015666-A2.  
PD 23-MAR-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 3; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 761  
ID AAB80219 standard; protein; 390 AA.  
DE Human PRO246 protein.  
PN WO200104311-A1.  
PD 18-JAN-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 4; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 762  
ID AAB31207 standard; protein; 390 AA.  
DE Amino acid sequence of human polypeptide PRO246.  
PN WO200077037-A2.  
PD 21-DEC-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 4; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 763  
ID AAB90818 standard; protein; 390 AA.  
DE Human shear stress-response protein SEQ ID NO: 144.  
PN WO200125427-A1.  
PD 12-APR-2001.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
PA (NOJI/) NOJIMA H.  
Query Match 16.1%; Score 307.5; DB 4; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 764  
ID AAU12340 standard; protein; 390 AA.  
DE Human PRO246 polypeptide sequence.  
PN WO200140466-A2.  
PD 07-JUN-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 4; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 765  
ID AAB53082 standard; protein; 390 AA.  
DE Human angiogenesis-associated protein PRO246, SEQ ID NO:96.  
PN WO200053753-A2.  
PD 14-SEP-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 4; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 766  
ID AAB68599 standard; protein; 390 AA.  
DE Amino acid sequence of protein PRO246.  
PN WO200105836-A1.  
PD 25-JAN-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 4; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 767  
ID AAB8358 standard; protein; 390 AA.  
DE Human membrane or secretory protein clone PSEC0086.  
PN EPI067182-A2.  
PD 10-JAN-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 16.1%; Score 307.5; DB 4; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 768  
ID ABU71597 standard; protein; 390 AA.  
DE Human PRO polypeptide #8.  
PN US2002146709-A1.  
PD 10-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 769  
ID ABO17784 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003032156-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 770  
ID ABU71452 standard; protein; 390 AA.  
DE Human PRO polypeptide #8.  
PN US2002192659-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 771  
ID ADA56949 standard; protein; 390 AA.  
DE Human secreted protein #232.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 772  
ID ABO25178 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003040014-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 773  
ID ABU81038 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003004311-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 774  
ID ABU71898 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein PRO246.  
PN US2003003530-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 775  
ID ABO01781 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.

PN US2002197671-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 776  
ID ABU66738 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003036180-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 777  
ID ASU54354 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein PRO246.  
PN US2002132240-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 778  
ID ADA40800 standard; protein; 390 AA.  
DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 779  
ID ABU67296 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003032063-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 780  
ID ABO47369 standard; protein; 390 AA.  
DE Human secreted/transmembrane polypeptide PRO246.  
PN US2003044839-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 781  
ID ABR47754 standard; protein; 390 AA.  
DE Human secreted protein, SEQ ID 645.  
PN WO200295010-A2.  
PD 28-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 782  
ID ABU59819 standard; protein; 390 AA.  
DE Novel secreted and transmembrane protein PRO246.  
PN US2003017563-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 783  
ID ABO25009 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein (PRO) #169.  
PN US2003036179-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 784  
ID ABU64506 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2002160374-A1.

PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 785  
ID ABU72064 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2002177165-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 786  
ID ABU67352 standard; protein; 390 AA.  
DE Human secreted protein PRO246.  
PN US2003023054-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 787  
ID ABU67165 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003032062-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 788  
ID ABO14872 standard; protein; 390 AA.  
DE Human secreted / transmembrane polypeptide PRO246.  
PN US2003036060-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 789  
ID ABU67014 standard; protein; 390 AA.  
DE Human secreted/transmembrane, PRO, protein SEQ ID 338.  
PN US2003032155-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 790  
ID ABU9629 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003017463-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 791  
ID ABU79807 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein PRO246.  
PN US2003032057-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 792  
ID ABO14811 standard; protein; 390 AA.  
DE Human secreted / transmembrane polypeptide PRO246.  
PN US2003027143-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 793  
ID ADA45857 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003022328-A1.  
PD 30-JAN-2003.

PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 794  
ID ADA76288 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003073212-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 795  
ID ADB29244 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003092002-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 796  
ID ADA18938 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003054517-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 797  
ID ADA61561 standard; protein; 390 AA.  
DE Homo sapiens.  
PN US2003049816-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 798  
ID ADB19346 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003068796-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 799  
ID ADB27887 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003082704-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 800  
ID ADA86366 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003082711-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 801  
ID ADB15930 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003087350-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 802  
ID ADA47716 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003073215-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 803  
ID ADA18100 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003039971-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 804  
ID ABO32763 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein PRO246.  
PN US2003045693-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 805  
ID ADA67511 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003068795-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 806  
ID ADB30518 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003068794-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 807  
ID ADA5814 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003082693-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 808  
ID ADA97026 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003082705-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 809  
ID ADA79330 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003082763-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 810  
ID ADA87469 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003087345-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 811  
ID ADB16671 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003087349-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 812  
ID ADA47716 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003073215-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.

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Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 812
ID ABO34317 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 813
ID ADA16075 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 814
ID ADA91763 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 815
ID ADB14826 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 816
ID ADA47282 standard; protein; 390 AA.
DE Human secreted/transmembrane polypeptide PRO246.
PN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 817
ID ADB18787 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 818
ID ADA94002 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 819
ID ADB19898 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 820
ID ADB13210 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 821
ID ABO43317 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 822
ID ADA74464 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 823
ID ADA42220 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 824
ID ADB24697 standard; protein; 390 AA.
DE Human PRO polypeptide SEQ ID NO 338.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 825
ID ADA82221 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 826
ID ADA75184 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 827
ID ADA85262 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 828
ID ADA84710 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 829
ID ABO17501 standard; protein; 390 AA.
DE Human PRO polypeptide #8.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 830
ID ABO17501 standard; protein; 390 AA.
DE Human PRO polypeptide #8.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
```

ID ADB29966 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003073214-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 831  
ID ADA80494 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003082761-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 832  
ID ADA75736 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003082703-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 833  
ID ADA6961 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003073210-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 834  
ID ADB25257 standard; protein; 390 AA.  
DE Human PRO polypeptide SEQ ID NO 338.  
PN US2003077715-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 835  
ID ADA93433 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003077721-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 836  
ID ADB26783 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003092147-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 837  
ID ADB31070 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003096386-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 838  
ID ADA60998 standard; protein; 390 AA.  
DE Homo sapiens.  
PN US2003049817-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 839  
ID ADB24145 standard; protein; 390 AA.

DE Human PRO polypeptide SEQ ID NO 338.  
PN US2003077714-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 840  
ID ADA96474 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003082690-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 841  
ID ADA81046 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003082702-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 842  
ID ADA95922 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003082759-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 843  
ID ADB26231 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003082760-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 844  
ID ADB21716 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003082765-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 6; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 845  
ID ADA77495 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003068797-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 846  
ID ADB18235 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003077710-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 847  
ID ADA86918 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003082709-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 848  
ID ADA16499 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.

PN US2003039969-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 849  
ID ADA12928 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003049622-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 850  
ID ADA41796 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003082540-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 851  
ID ADA88021 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003082700-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 852  
ID ADA46409 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003054516-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 853  
ID ADA17143 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003017498-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 854  
ID ADA42646 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003054351-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 855  
ID ADB28439 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003082699-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 856  
ID ADB28991 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003082706-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 857  
ID ADA76943 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003059909-A1.

PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 858  
ID ADA88573 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003073213-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 859  
ID ADA97578 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003082686-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 860  
ID ADB27335 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003022239-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 861  
ID ADB22268 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003087344-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 862  
ID ABO19865 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein PRO246.  
PN US2003044902-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 863  
ID ABO17562 standard; protein; 390 AA.  
DE Human PRO polypeptide #8.  
PN US2003064923-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 864  
ID ADA68959 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003068793-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 865  
ID ADB22820 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003077711-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 866  
ID ADB23593 standard; protein; 390 AA.  
DE Human PRO polypeptide SEQ ID NO 338.  
PN US2003077712-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;



Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 867  
ID ADB74701 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003082542-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 868  
ID ADB15378 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003087352-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 869  
ID ADB38630 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003082766-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 870  
ID ADB38078 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003087347-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 871  
ID ADB66550 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003082689-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 872  
ID ADB89630 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003082698-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 873  
ID ADB90362 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003082762-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 874  
ID ADB77565 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003077654-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 875  
ID ADB39463 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003082764-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 876  
ID ADB74701 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003082542-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 877  
ID ADB47086 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003082687-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 878  
ID ADB86693 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003082697-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 879  
ID ADB77298 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003082696-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 880  
ID ADB34455 standard; protein; 390 AA.  
DE Human PRO polypeptide SEQ ID NO 338.  
PN US2003077717-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 881  
ID ADB35559 standard; protein; 390 AA.  
DE Human PRO polypeptide SEQ ID NO 338.  
PN US2003077719-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 882  
ID ADB33903 standard; protein; 390 AA.  
DE Human PRO polypeptide SEQ ID NO 338.  
PN US2003077716-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 883  
ID ADB35007 standard; protein; 390 AA.  
DE Human PRO polypeptide SEQ ID NO 338.  
PN US2003077718-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 884  
ID ADB36111 standard; protein; 390 AA.  
DE Human PRO polypeptide SEQ ID NO 338.  
PN US2003077720-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 885

ID ADB46506 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003082692-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 886  
ID ADC28347 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003059772-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 887  
ID ADC39547 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003059828-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 888  
ID ADC40061 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003059829-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 889  
ID ADC18889 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003036061-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 890  
ID ADC34185 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003036094-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 891  
ID ADC29240 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003049676-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 892  
ID ADC28771 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003049677-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 893  
ID ADC40656 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003054400-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 894  
ID ADC19313 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.

DE Human secreted/transmembrane protein, #9.  
PN US2003054441-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 895  
ID ADC33761 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003073077-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 896  
ID ADC12831 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003073079-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 897  
ID ADC50379 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003092106-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 898  
ID ADC71926 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003092107-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 899  
ID ADC59905 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003092105-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 900  
ID ADC52912 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein Seq ID338.  
PN US2003087365-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 901  
ID ADC57266 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein Seq ID338.  
PN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 902  
ID ADC60457 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 903  
ID ADC50932 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.

PN US2003087361-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 904  
ID ADC65459 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003087362-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 905  
ID ADC54557 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein Seq ID338.  
PN US2003087363-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 906  
ID ADC53518 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein Seq ID338.  
PN US2003087364-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 907  
ID ADC59041 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein Seq ID338.  
PN US2003087359-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 908  
ID ADC55919 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein Seq ID338.  
PN US2003087360-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 909  
ID ADC58489 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein Seq ID338.  
PN US2003087346-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 910  
ID ADC12283 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003082541-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 911  
ID ADD03163 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003092104-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 912  
ID ADC90155 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003087348-A1.

PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 913  
ID ADC69574 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003194770-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 914  
ID ADC48463 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003194773-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 915  
ID ADD09992 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003194776-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 916  
ID ADD04567 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003087354-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 917  
ID ADC80523 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003092103-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 918  
ID ADD11030 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003194774-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 919  
ID ADC47911 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003194771-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 920  
ID ADD04838 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003104469-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 921  
ID ADC79971 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003087358-A1.  
PD 08-MAY-2003.

PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 922  
ID ADD09440 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003194775-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 923  
ID ADD03844 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003104381-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 924  
ID ADD03420 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003108983-A1.  
PD 12-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 925  
ID ADD41153 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003203438-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 926  
ID ADD52292 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003194769-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 927  
ID ADD53032 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003194792-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 928  
ID ADD53584 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003203437-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 929  
ID ADD51740 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003194779-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 930  
ID ADD02539 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003203431-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.

Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 931  
ID ADD01973 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003203430-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 932  
ID ADD54155 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003203432-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 933  
ID ADD92472 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003199030-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 934  
ID ADD91368 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003199055-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 935  
ID ADE03982 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003199057-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 936  
ID ADE32279 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003194765-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 937  
ID ADE22211 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003199056-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 938  
ID ADD79435 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003203428-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 939  
ID ADE41971 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003194772-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;

Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 940  
ID ADE17788 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003199023-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 941  
ID ADD91920 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003199053-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 942  
ID ADE33383 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003194767-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 943  
ID ADE33935 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003194791-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 944  
ID ADD79987 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003207417-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 945  
ID ADD93024 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003194768-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 946  
ID ADE19444 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003199025-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 947  
ID ADE34672 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003077583-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 948  
ID ADE18892 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003199026-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 949  
ID ADE43088 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003199033-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 950  
ID ADD95877 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003199059-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 951  
ID ADE22763 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003199064-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 952  
ID ADD78881 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003203429-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 953  
ID ADE32831 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003194766-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 954  
ID ADE42523 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003199032-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 955  
ID ADD80539 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003207418-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 956  
ID ADD89567 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003199028-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 957  
ID ADE40851 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003199031-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 958  
ID ADE40851 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003199031-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 959

ID ADE04650 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003199034-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 959  
ID ADE92779 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003194777-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 960  
ID ADG21488 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207355-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 961  
ID ADG23129 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207384-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 962  
ID ADP97464 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003207370-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 963  
ID ADG80528 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003207373-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 964  
ID ADG79976 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003207372-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 965  
ID ADG63791 standard; protein; 390 AA.  
DE Human secreted/transmembrane polypeptide PRO246.  
PN US2003170721-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 966  
ID ADH59155 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003039972-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 967  
ID ADH55268 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207381-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 968  
ID ADH55820 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207379-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 969  
ID ADI37934 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003054352-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 970  
ID ADI64039 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207385-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 971  
ID ADI64988 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207386-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 972  
ID ADI63487 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207387-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 973  
ID ADH81901 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207388-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 974  
ID ADH81349 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207377-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 975  
ID ADJ26202 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003054349-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 976  
ID ADM82518 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.

PN US2003087355-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 977  
ID ADN15917 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003087353-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 978  
ID ADN16546 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003087385-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 979  
ID ADN15365 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003087356-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 980  
ID ADN14813 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003087357-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 7; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 981  
ID ADC81075 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003092115-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 982  
ID ADE79117 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003135025-A1.  
PD 17-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 983  
ID ADD76523 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003100087-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 984  
ID ADD87887 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003092113-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 985  
ID ADD86291 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003203440-A1.

PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 986  
ID ADE79541 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003130489-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 987  
ID ADE75739 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003211571-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 988  
ID ADE73217 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003129592-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 989  
ID ADE23315 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003092108-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 990  
ID ADE23867 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003092110-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 991  
ID ADE24510 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003092111-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 992  
ID ADD87335 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003203439-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 993  
ID ADE89201 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003199062-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 994  
ID ADE41205 standard; protein; 390 AA.  
DE Human secreted/transmembrane polypeptide PRO246.  
PN US2003104558-A1.  
PD 05-JUN-2003.

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PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 995
ID ADE73752 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 996
ID ADE18340 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 997
ID ADE88649 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 998
ID ADE99306 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 999
ID ADE94669 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1000
ID ADE91080 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1001
ID ADE95221 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1002
ID ADE93331 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1003
ID ADE34912 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1004
ID ADE98425 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1005
ID ADE92227 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1006
ID ADE90528 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1007
ID ADE91675 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1008
ID ADE98852 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1009
ID ADG40322 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003235253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1010
ID ADF73716 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1011
ID ADG02254 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1012
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ID ADG22040 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
FN US2003207360-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1013  
ID ADG20110 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
FN US2003207376-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1014  
ID ADF98016 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
FN US2003207422-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1015  
ID ADF98587 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
FN US2003208055-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1016  
ID ADF98587 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
FN US2003208055-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1017  
ID ADG03418 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
FN US2003207351-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1018  
ID ADF99139 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
FN US2003207353-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1019  
ID ADG16724 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
FN US2003207359-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1020  
ID ADG05183 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
FN US2003207375-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1021  
ID ADG19450 standard; protein; 390 AA.

DE Human PRO polypeptide #169.  
FN US2003207425-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1022  
ID ADF73292 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
FN US2003166051-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1023  
ID ADG13287 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
FN US2003207357-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1024  
ID ADG08344 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
FN US2003207424-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1025  
ID ADG15514 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
FN US2003219885-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1026  
ID ADF96912 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
FN US2003207371-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1027  
ID ADG06097 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
FN US2003207374-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1028  
ID ADG23681 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
FN US2003207389-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1029  
ID ADG03970 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
FN US2003207423-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1030  
ID ADG24871 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.

PN US2003207427-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1031  
ID ADG07168 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207350-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1032  
ID ADG07720 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207356-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1033  
ID ADG59215 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003194778-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1034  
ID ADG60879 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207390-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1035  
ID ADG61983 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207428-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1036  
ID ADG92135 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003027145-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1037  
ID ADG82184 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003207358-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1038  
ID ADG57423 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207362-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1039  
ID ADG56871 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207364-A1.

PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1040  
ID ADG55767 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207365-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1041  
ID ADG58527 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207368-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1042  
ID ADG70893 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207420-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1043  
ID ADG92562 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003027146-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1044  
ID ADG57975 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207363-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1045  
ID ADG53559 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207415-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1046  
ID ADG71445 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207421-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1047  
ID ADG81632 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003207805-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1048  
ID ADH30594 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003077723-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1049  
ID ADG63640 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane polypeptide PRO246.  
PN US2003180796-A1.  
PD 25-SEP-2003  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1050  
ID ADH11961 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207419-A1.  
PD 06-NOV-2003  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1051  
ID ADG52383 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207414-A1.  
PD 06-NOV-2003  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1052  
ID ADG54111 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207416-A1.  
PD 06-NOV-2003  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1053  
ID ADG81080 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003194793-A1.  
PD 16-OCT-2003  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1054  
ID ADG56319 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207366-A1.  
PD 06-NOV-2003  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1055  
ID ADH12585 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207378-A1.  
PD 06-NOV-2003  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1056  
ID ADG61431 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207429-A1.  
PD 06-NOV-2003  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1057  
ID ADH28518 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003022331-A1.  
PD 30-JAN-2003  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;

Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1058  
ID ADG54663 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207367-A1.  
PD 06-NOV-2003  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1059  
ID ADG59703 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207369-A1.  
PD 06-NOV-2003  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1060  
ID ADH20351 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2004005553-A1.  
PD 08-JAN-2004  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1061  
ID ADH07206 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2004006211-A1.  
PD 08-JAN-2004  
PA (DESN/) DESNOYERS L.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHER J P.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1062  
ID ADH59751 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003215904-A1.  
PD 20-NOV-2003  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1063  
ID ADH06779 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2004005665-A1.  
PD 08-JAN-2004  
PA (DESN/) DESNOYERS L.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHER J P.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1064  
ID ADI81127 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2003207361-A1.  
PD 06-NOV-2003  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1065  
ID ADI18521 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003152999-A1.

PD 14-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1066  
ID ADI65241 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003148419-A1.  
PD 07-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1067  
ID ADI37504 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003096340-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1068  
ID ADG09870 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2004009548-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1069  
ID ADH97308 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003190610-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1070  
ID ADI15341 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207382-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1071  
ID ADG09218 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2004009547-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1072  
ID ADI65668 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003148371-A1.  
PD 07-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1073  
ID ADI14673 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207383-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1074  
ID ADH60411 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2004023331-A1.  
PD 05-FEB-2004.

PA (DESN/) DESNOYERS L.  
PA (GODO/) GODDARD A.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHER J P.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1075  
ID ADI18268 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2003207349-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1076  
ID ADJ99468 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003187238-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1077  
ID ADL08661 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003186358-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1078  
ID ADM25006 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003096233-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1079  
ID ADJ63549 standard; protein; 390 AA.  
DE Novel human secreted and transmembrane protein PRO246.  
PN US2004039164-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1080  
ID ADM29752 standard; protein; 390 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2003190611-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1081  
ID ADJ77444 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2004038336-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;  
RESULT 1082  
ID ADJ65566 standard; protein; 390 AA.  
DE Human PRO polypeptide #169.  
PN US2004038335-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 16.1%; Score 307.5; DB 8; Length 390;  
Best Local Similarity 29.2%; Pred. No. 4.4e-16;

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RESULT 1083
ID ADM27702 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1084
ID ADM42426 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2004058424-A1.
PD 23-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1085
ID ADO06074 standard; protein; 390 AA.
DE Human PRO polypeptide #8.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1086
ID ADM28288 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1087
ID ADR10926 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1088
ID ADR17835 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1089
ID ADI95770 standard; protein; 390 AA.
DE Human PRO polypeptide #169.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1090
ID ADI96322 standard; protein; 390 AA.
DE Novel human secreted and transmembrane protein PRO246.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1091
ID ADT03511 standard; protein; 390 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1092
ID ADS74474 standard; protein; 390 AA.
DE Human secreted/transmembrane protein #9.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 16.1%; Score 307.5; DB 8; Length 390;
Best Local Similarity 29.2%; Pred. No. 4.4e-16;
RESULT 1093
ID ABO53064 standard; protein; 390 AA.
DE Human putative spliceosome associated protein (SAP) #41.
PN US2003068803-A1.
PD 10-APR-2003.
PA (REED/) REED R.
PA (ZHOU/) ZHOU Z.
Query Match 16.0%; Score 305.5; DB 6; Length 390;
Best Local Similarity 29.2%; Pred. No. 6.4e-16;
RESULT 1094
ID AAY08073 standard; protein; 268 AA.
DE Human A33 protein.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH ) GENENTECH INC.
Query Match 16.0%; Score 304.5; DB 2; Length 268;
Best Local Similarity 31.9%; Pred. No. 4.6e-16;
RESULT 1095
ID ADH62551 standard; protein; 268 AA.
DE Human A33 antigenic protein fragment #1.
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PN US2003171568-A1.  
PD 11-SEP-2003.  
PA (ASHK/) ASHKENAZI A.  
PA (FONG/) FONG S.  
PA (GODD/) GODDARD A.  
PA (GURN/) GURNEY A L.  
PA (NAPI/) NAPIER M A.  
PA (TUMA/) TUMAS D.  
PA (WOOD/) WOOD W I.  
Query Match 16.0%; Score 304.5; DB 7; Length 268;  
Best Local Similarity 31.9%; Pred. No. 4.6e-16;  
RESULT 1096  
ID AAY23327 standard; protein; 270 AA.  
DE An A33 related antigen sequence.  
PN WO9927098-A2.  
PD 03-JUN-1999.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 304.5; DB 2; Length 270;  
Best Local Similarity 31.9%; Pred. No. 4.6e-16;  
RESULT 1097  
ID AAY23329 standard; protein; 273 AA.  
DE An A33 related antigen sequence.  
PN WO9927098-A2.  
PD 03-JUN-1999.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 304.5; DB 2; Length 273;  
Best Local Similarity 31.9%; Pred. No. 4.7e-16;  
RESULT 1098  
ID AAY08075 standard; protein; 273 AA.  
DE Human A33 protein fragment #2.  
PN WO9914241-A2.  
PD 25-MAR-1999.  
PA (GETH ) GENENTECH INC.  
Query Match 16.0%; Score 304.5; DB 2; Length 273;  
Best Local Similarity 31.9%; Pred. No. 4.7e-16;  
RESULT 1099  
ID ADH62553 standard; protein; 273 AA.  
DE Human A33 antigenic protein fragment #2.  
PN US2003171568-A1.  
PD 11-SEP-2003.  
PA (ASHK/) ASHKENAZI A.  
PA (FONG/) FONG S.  
PA (GODD/) GODDARD A.  
PA (GURN/) GURNEY A L.  
PA (NAPI/) NAPIER M A.  
PA (TUMA/) TUMAS D.  
PA (WOOD/) WOOD W I.  
Query Match 16.0%; Score 304.5; DB 7; Length 273;  
Best Local Similarity 31.9%; Pred. No. 4.7e-16;  
RESULT 1100  
ID ABB11937 standard; peptide; 321 AA.  
DE Human viral receptor protein homologue, SEQ ID NO:2307.  
PN WO200157188-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 15.9%; Score 303.5; DB 4; Length 321;  
Best Local Similarity 30.2%; Pred. No. 7e-16;  
RESULT 1101  
ID AAM40551 standard; protein; 321 AA.  
DE Human polypeptide SEQ ID NO 5482.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 15.9%; Score 303.5; DB 4; Length 321;  
Best Local Similarity 30.2%; Pred. No. 7e-16;  
RESULT 1102  
ID ADS11818 standard; protein; 321 AA.  
DE Human therapeutic contig protein - SEQ ID 2055.  
PN WO2004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 15.9%; Score 303.5; DB 8; Length 321;  
Best Local Similarity 30.2%; Pred. No. 7e-16;  
RESULT 1103  
ID AAB08903 standard; protein; 327 AA.  
DE Human secreted protein sequence encoded by gene 13 SEQ ID NO:60.  
PN WO200017222-A1.  
PD 30-MAR-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 15.9%; Score 303.5; DB 3; Length 327;  
Best Local Similarity 29.9%; Pred. No. 7.2e-16;  
RESULT 1104  
ID ADB64882 standard; protein; 317 AA.  
DE Human protein encoded by clone PLACE60070500.  
PN EPI308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 15.9%; Score 303; DB 7; Length 317;  
Best Local Similarity 29.9%; Pred. No. 7.6e-16;  
RESULT 1105  
ID ADE08316 standard; protein; 538 AA.  
DE Novel protein (useful for identifying genetic disorders) #471.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 15.8%; Score 302; DB 7; Length 538;  
Best Local Similarity 25.9%; Pred. No. 1.9e-15;  
RESULT 1106  
ID AAE06610 standard; protein; 390 AA.  
DE Human protein having hydrophobic domain, HP10801.  
PN WO200149728-A2.  
PD 12-JUL-2001.  
PA (PROT-) PROTEGENE INC.  
PA (SAGA ) SAGAMI CHEM RES CENT.  
Query Match 15.7%; Score 299.5; DB 4; Length 390;  
Best Local Similarity 28.9%; Pred. No. 1.9e-15;  
RESULT 1107  
ID ADM05828 standard; protein; 406 AA.  
DE Human protein of the invention SEQ ID NO:4513.  
PN EPI347046-A1.  
PD 24-SRP-2003.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 15.5%; Score 296.5; DB 7; Length 406;  
Best Local Similarity 27.1%; Pred. No. 3.6e-15;  
RESULT 1108  
ID ADO43535 standard; protein; 348 AA.  
DE Amino acid sequence of an additional human A34 clone.  
PN WO2004037999-A2.  
PD 06-MAY-2004.  
PA (LUDW-) LUDWIG INST CANCER RES.  
Query Match 15.5%; Score 295; DB 8; Length 348;  
Best Local Similarity 26.6%; Pred. No. 3.8e-15;  
RESULT 1109  
ID ADP55948 standard; protein; 370 AA.  
DE Human PRO protein sequence SEQ ID NO:1924.  
PN WO2004039956-A2.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 15.5%; Score 295; DB 8; Length 370;  
Best Local Similarity 26.6%; Pred. No. 4.2e-15;  
RESULT 1110  
ID AAY08621 standard; protein; 387 AA.  
DE Human secreted protein AJ26\_3.  
PN WO9926972-A1.  
PD 03-JUN-1999.  
PA (GEMY ) GENETICS INST INC.  
Query Match 15.5%; Score 295; DB 2; Length 387;  
Best Local Similarity 26.6%; Pred. No. 4.4e-15;  
RESULT 1111  
ID AAY67312 standard; protein; 387 AA.  
DE Human secreted protein AJ26\_3 amino acid sequence.  
PN WO9960020-A1.  
PD 25-NOV-1999.  
PA (GEMY ) GENETICS INST INC.  
Query Match 15.5%; Score 295; DB 3; Length 387;  
Best Local Similarity 26.6%; Pred. No. 4.4e-15;

Best Local Similarity 26.6%; Pred. No. 4.4e-15;  
RESULT 1112  
ID ADC38775 standard; protein; 387 AA.  
DE Human secreted protein #62.  
PN US2002193567-A1.  
PD 19-DEC-2002.  
PA (GEMY) GENETICS INST INC.  
Query Match 15.5%; Score 295; DB 7; Length 387;  
Best Local Similarity 26.6%; Pred. No. 4.4e-15;  
RESULT 1113  
ID ADO43531 standard; protein; 387 AA.  
DE Amino acid sequence of a full length human A34 protein.  
PN WO2004037999-A2.  
PD 06-MAY-2004.  
PA (LUDW-) LUDWIG INST CANCER RES.  
Query Match 15.5%; Score 295; DB 8; Length 387;  
Best Local Similarity 26.6%; Pred. No. 4.4e-15;  
RESULT 1114  
ID ADO43533 standard; protein; 402 AA.  
DE Amino acid sequence of a human A34 protein.  
PN WO2004037999-A2.  
PD 06-MAY-2004.  
PA (LUDW-) LUDWIG INST CANCER RES.  
Query Match 15.5%; Score 295; DB 8; Length 402;  
Best Local Similarity 26.6%; Pred. No. 4.7e-15;  
RESULT 1115  
ID ADO65260 standard; protein; 407 AA.  
DE Novel human protein sequence #233.  
PN EP1440981-A2.  
PD 28-JUL-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 15.5%; Score 295; DB 8; Length 407;  
Best Local Similarity 27.5%; Pred. No. 4.7e-15;  
RESULT 1116  
ID ABM84859 standard; protein; 344 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5108.  
PN WO2004023573-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 15.4%; Score 294; DB 8; Length 344;  
Best Local Similarity 29.3%; Pred. No. 4.5e-15;  
RESULT 1117  
ID ADC42841 standard; protein; 423 AA.  
DE REMAP protein #1.  
PN WO2003027228-A2.  
PD 03-APR-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 15.3%; Score 291; DB 7; Length 423;  
Best Local Similarity 24.4%; Pred. No. 1e-14;  
RESULT 1118  
ID ADP29419 standard; protein; 244 AA.  
DE Human secreted protein SEQ ID #186.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 15.1%; Score 288.5; DB 8; Length 244;  
Best Local Similarity 28.3%; Pred. No. 7.8e-15;  
RESULT 1119  
ID AAB85732 standard; protein; 192 AA.  
DE Rat coxsackie-adenovirus receptor (CAR).  
PN JP2001149095-A.  
PD 05-JUN-2001.  
PA (KAGA-) KAGAKU GIJUTSU SHINKO KI.  
PA (HIRO-) ZH HIROSHIMAKEN SANGYO GIJUTSU SHINKO KI.  
Query Match 15.1%; Score 288; DB 4; Length 192;  
Best Local Similarity 33.5%; Pred. No. 6.2e-15;  
RESULT 1120  
ID ADC78359 standard; protein; 389 AA.  
DE Human PRO246 protein.  
PN WO200015796-A2.  
PD 23-MAR-2000.  
PA (GETH) GENENTECH INC.  
Query Match 15.1%; Score 287.5; DB 3; Length 389;

Best Local Similarity 28.2%; Pred. No. 1.8e-14;  
RESULT 1121  
ID ADN39990 standard; protein; 413 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C360.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 14.9%; Score 285; DB 7; Length 413;  
Best Local Similarity 25.7%; Pred. No. 3.1e-14;  
RESULT 1122  
ID ADR46674 standard; protein; 413 AA.  
DE Cancer-associated protein, SEQ ID 87.  
PN WO2004073657-A2.  
PD 02-SEP-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 14.9%; Score 285; DB 8; Length 413;  
Best Local Similarity 25.7%; Pred. No. 3.1e-14;  
RESULT 1123  
ID ADN39989 standard; protein; 631 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C359.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 14.9%; Score 285; DB 7; Length 631;  
Best Local Similarity 25.7%; Pred. No. 5.5e-14;  
RESULT 1124  
ID ADR46673 standard; protein; 631 AA.  
DE Cancer-associated protein, SEQ ID 86.  
PN WO2004073657-A2.  
PD 02-SEP-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 14.9%; Score 285; DB 8; Length 631;  
Best Local Similarity 25.7%; Pred. No. 5.5e-14;  
RESULT 1125  
ID ADP30373 standard; protein; 377 AA.  
DE Human secreted protein SEQ ID #1140.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 14.9%; Score 284.5; DB 8; Length 377;  
Best Local Similarity 26.6%; Pred. No. 3e-14;  
RESULT 1126  
ID AAB65905 standard; protein; 370 AA.  
DE Human secreted protein related protein SEQ ID NO: 136.  
PN WO200078808-A1.  
PD 28-DEC-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 14.4%; Score 275; DB 4; Length 370;  
Best Local Similarity 29.6%; Pred. No. 1.7e-13;  
RESULT 1127  
ID ADO43537 standard; protein; 370 AA.  
DE Amino acid sequence of a human A33-like 3 protein.  
PN WO2004037999-A2.  
PD 06-MAY-2004.  
PA (LUDW-) LUDWIG INST CANCER RES.  
Query Match 14.4%; Score 274; DB 8; Length 370;  
Best Local Similarity 29.6%; Pred. No. 2e-13;  
RESULT 1128  
ID AAW14158 standard; protein; 318 AA.  
DE Mouse A33 antigen.  
PN WO9708189-A1.  
PD 06-MAR-1997.  
PA (LUDW-) LUDWIG INST CANCER RES.  
Query Match 14.3%; Score 272.5; DB 2; Length 318;  
Best Local Similarity 28.8%; Pred. No. 2.2e-13;  
RESULT 1129  
ID AAB65833 standard; protein; 341 AA.  
DE Murine mature INTERCEPT 258 SEQ ID NO: 29.  
PN WO200078808-A1.  
PD 28-DEC-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 14.2%; Score 271; DB 4; Length 341;  
Best Local Similarity 29.3%; Pred. No. 3.2e-13;

RESULT 1130  
ID AAB65832 standard; protein; 370 AA.  
DE Human INTERCEPT 258 SEQ ID NO: 28.  
PN WO200078808-A1.  
PD 28-DEC-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 14.2%; Score 271; DB 4; Length 370;  
Best Local Similarity 29.3%; Pred. No. 3.6e-13;  
RESULT 1131  
ID AAB65904 standard; protein; 370 AA.  
DE Human secreted protein related protein SEQ ID NO: 134.  
PN WO200078808-A1.  
PD 28-DEC-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 14.2%; Score 271; DB 4; Length 370;  
Best Local Similarity 29.3%; Pred. No. 3.6e-13;  
RESULT 1132  
ID AAB65907 standard; protein; 370 AA.  
DE Human secreted protein related protein SEQ ID NO: 140.  
PN WO200078808-A1.  
PD 28-DEC-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 14.2%; Score 270; DB 4; Length 370;  
Best Local Similarity 29.3%; Pred. No. 4.3e-13;  
RESULT 1133  
ID AAB65906 standard; protein; 370 AA.  
DE Human secreted protein related protein SEQ ID NO: 138.  
PN WO200078808-A1.  
PD 28-DEC-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 14.1%; Score 269; DB 4; Length 370;  
Best Local Similarity 29.0%; Pred. No. 5.2e-13;  
RESULT 1134  
ID AAU18038 standard; protein; 294 AA.  
DE Human immunoglobulin polypeptide SEQ ID No 183.  
PN WO200155315-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 13.9%; Score 265; DB 4; Length 294;  
Best Local Similarity 32.2%; Pred. No. 7.9e-13;  
RESULT 1135  
ID ADB31662 standard; protein; 294 AA.  
DE Human novel protein SEQ ID NO 183.  
PN US2003077606-A1.  
PD 24-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 13.9%; Score 265; DB 7; Length 294;  
Best Local Similarity 32.2%; Pred. No. 7.9e-13;  
RESULT 1136  
ID ADO43538 standard; protein; 228 AA.  
DE Amino acid sequence of a human A33-like 3 protein fragment.  
PN WO2004037999-A2.  
PD 06-MAY-2004.  
PA (LUDW-) LUDWIG INST CANCER RES.  
Query Match 13.0%; Score 247.5; DB 8; Length 228;  
Best Local Similarity 29.5%; Pred. No. 1.4e-11;  
RESULT 1137  
ID ADM87310 standard; protein; 273 AA.  
DE Human protein SEQ ID NO:403.  
PN WO2004009834-A2.  
PD 29-JAN-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 12.7%; Score 242.5; DB 8; Length 273;  
Best Local Similarity 31.8%; Pred. No. 4.7e-11;  
RESULT 1138  
ID ADN02700 standard; protein; 205 AA.  
DE Human receptor and membrane -associated protein #3.  
PN WO2004029218-A2.  
PD 08-APR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 12.3%; Score 235; DB 8; Length 205;  
Best Local Similarity 33.5%; Pred. No. 1.3e-10;  
RESULT 1139  
ID AAB08940 standard; protein; 245 AA.  
DE Human secreted protein sequence encoded by gene 13 SEQ ID NO:97.  
PN WO200017222-A1.  
PD 30-MAR-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 12.0%; Score 228.5; DB 3; Length 245;  
Best Local Similarity 29.3%; Pred. No. 5.4e-10;  
RESULT 1140  
ID AAB08926 standard; protein; 246 AA.  
DE Human secreted protein sequence encoded by gene 13 SEQ ID NO:83.  
PN WO200017222-A1.  
PD 30-MAR-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 12.0%; Score 228.5; DB 3; Length 246;  
Best Local Similarity 29.3%; Pred. No. 5.4e-10;  
RESULT 1141  
ID ADL67138 standard; protein; 242 AA.  
DE Human B7-H5(ECD) protein SEQ ID NO:8.  
PN WO2004022594-A2.  
PD 18-MAR-2004.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Query Match 11.9%; Score 227; DB 8; Length 242;  
Best Local Similarity 31.0%; Pred. No. 7e-10;  
RESULT 1142  
ID ADR20065 standard; protein; 346 AA.  
DE Human immune response associated protein (IRAP), seq id 25.  
PN WO2004048550-A2.  
PD 10-JUN-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 11.9%; Score 226.5; DB 8; Length 346;  
Best Local Similarity 24.0%; Pred. No. 1.3e-09;  
RESULT 1143  
ID ADL67142 standard; protein; 238 AA.  
DE Mouse B7-H5(ECD) protein SEQ ID NO:12.  
PN WO2004022594-A2.  
PD 18-MAR-2004.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Query Match 11.8%; Score 225.5; DB 8; Length 238;  
Best Local Similarity 30.4%; Pred. No. 9.1e-10;  
RESULT 1144  
ID ABP41477 standard; protein; 226 AA.  
DE Human ovarian antigen HOPNF21, SEQ ID NO:2609.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.2%; Score 214; DB 5; Length 226;  
Best Local Similarity 29.5%; Pred. No. 7.2e-09;  
RESULT 1145  
ID AAB61417 standard; protein; 162 AA.  
DE Human TANGO 244 protein.  
PN WO200100672-A1.  
PD 04-JAN-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.9%; Score 207.5; DB 4; Length 162;  
Best Local Similarity 34.8%; Pred. No. 1.5e-08;  
RESULT 1146  
ID AAB65843 standard; protein; 249 AA.  
DE Murine INTERCEPT 258 extracellular domain SEQ ID NO: 42.  
PN WO200078808-A1.  
PD 28-DEC-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.6%; Score 202; DB 4; Length 249;  
Best Local Similarity 27.1%; Pred. No. 7.6e-08;  
RESULT 1147  
ID AAO16453 standard; protein; 310 AA.  
DE Human junctional adhesion molecule 3 (huJAM3).  
PN WO2003008541-A2.  
PD 30-JAN-2003.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 10.4%; Score 198.5; DB 6; Length 310;  
Best Local Similarity 26.7%; Pred. No. 2e-07;  
RESULT 1148  
ID AAY96294 standard; protein; 310 AA.



DE Human IGFAM-6 immunoglobulin.  
PN WO200029583-A2.  
PD 25-MAY-2000.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 10.4%; Score 197.5; DB 3; Length 310;  
Best Local Similarity 26.7%; Pred. No. 2.4e-07;  
RESULT 1149  
ID ADP56683 standard; protein; 310 AA.  
DE Human junction adhesion molecule 3 (hJAM3) full-length protein.  
PN WO2004053058-A2.  
PD 24-JUN-2004.  
PA (EIL) LILLY & CO ELI.  
Query Match 10.4%; Score 197.5; DB 8; Length 310;  
Best Local Similarity 26.7%; Pred. No. 2.4e-07;  
RESULT 1150  
ID AAY08071 standard; protein; 299 AA.  
DE Human PRO307 protein.  
PN WO9914241-A2.  
PD 25-MAR-1999.  
PA (GETH) GENENTECH INC.  
Query Match 10.3%; Score 197; DB 2; Length 299;  
Best Local Similarity 24.8%; Pred. No. 2.5e-07;  
RESULT 1151  
ID AAY23321 standard; protein; 299 AA.  
DE Amino acid sequence of the PRO301 polypeptide.  
PN WO9927098-A2.  
PD 03-JUN-1999.  
PA (GETH) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 2; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1152  
ID AAW74464 standard; protein; 299 AA.  
DE Fil antigen protein sequence.  
PN WO9902561-A1.  
PD 21-JAN-1999.  
PA (SWIK) SMITHKLINE BEECHAM CORP.  
Query Match 10.3%; Score 196; DB 2; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1153  
ID AAY13364 standard; protein; 299 AA.  
DE Amino acid sequence of protein PRO301.  
PN WO9914328-A2.  
PD 25-MAR-1999.  
PA (GETH) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 2; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1154  
ID AAY76011 standard; protein; 299 AA.  
DE Human A33 receptor homologue, SEQ ID NO:189.  
PN WO9955865-A1.  
PD 04-NOV-1999.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Query Match 10.3%; Score 196; DB 3; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1155  
ID AAY76076 standard; protein; 299 AA.  
DE Human A33 receptor homologue, SEQ ID NO:331.  
PN WO9955865-A1.  
PD 04-NOV-1999.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Query Match 10.3%; Score 196; DB 3; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1156  
ID AAY70670 standard; protein; 299 AA.  
DE Human PRO301 protein.  
PN WO200015797-A2.  
PD 23-MAR-2000.  
PA (GETH) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 3; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1157  
ID AAB24405 standard; protein; 299 AA.  
DE Human PRO301 protein sequence SEQ ID NO:90.  
PN WO200053753-A2.

PN WO200032221-A2.  
PD 08-JUN-2000.  
PA (GETH) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 3; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1158  
ID AAY95344 standard; protein; 299 AA.  
DE Human PRO301 antitumour protein.  
PN WO200037638-A2.  
PD 29-JUN-2000.  
PA (GETH) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 3; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1159  
ID AAB80232 standard; protein; 299 AA.  
DE Human PRO301 protein.  
PN WO200104311-A1.  
PD 18-JAN-2001.  
PA (GETH) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 4; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1160  
ID AAM93577 standard; protein; 299 AA.  
DE Human polypeptide, SEQ ID NO: 3365.  
PN EP1130094-A2.  
PD 05-SEP-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 10.3%; Score 196; DB 4; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1161  
ID AAB56015 standard; protein; 299 AA.  
DE Skin cell protein, SEQ ID NO: 331.  
PN WO200069884-A2.  
PD 23-NOV-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Query Match 10.3%; Score 196; DB 4; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1162  
ID AAB55950 standard; protein; 299 AA.  
DE Skin cell protein, SEQ ID NO: 189.  
PN WO200069884-A2.  
PD 23-NOV-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Query Match 10.3%; Score 196; DB 4; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1163  
ID AAB31202 standard; protein; 299 AA.  
DE Amino acid sequence of human polypeptide PRO301.  
PN WO200077037-A2.  
PD 21-DEC-2000.  
PA (GETH) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 4; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1164  
ID AAU00823 standard; protein; 299 AA.  
DE Human immune response protein PRO301 (UNQ364).  
PN WO200119991-A1.  
PD 22-MAR-2001.  
PA (GETH) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 4; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1165  
ID AAU12354 standard; protein; 299 AA.  
DE Human PRO301 polypeptide sequence.  
PN WO200140466-A2.  
PD 07-JUN-2001.  
PA (GETH) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 4; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1166  
ID AAB53086 standard; protein; 299 AA.  
DE Human angiogenesis-associated protein PRO301, SEQ ID NO:119.  
PN WO200053753-A2.



Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1183  
ID ABO25173 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
FN US2003040014-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1184  
ID ABU81052 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
FN US2003004311-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1185  
ID ABU71911 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein PRO301.  
FN US2003003530-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1186  
ID ABO01794 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
FN US2002197671-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1187  
ID ABU66752 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
FN US2003036180-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1188  
ID ABU54367 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein PRO301.  
FN US2002132240-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1189  
ID ABU67291 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
FN US2003032063-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1190  
ID ABO47382 standard; protein; 299 AA.  
DE Human secreted/transmembrane polypeptide PRO301.  
FN US2003044839-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1191  
ID ABU59833 standard; protein; 299 AA.  
DE Novel secreted and transmembrane protein PRO301.  
FN US2003017563-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1192  
ID ABO25023 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein (PRO) #183.  
FN US2003036179-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1193  
ID ABU64519 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #23.  
FN US2002160374-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1194  
ID ABU72059 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
FN US2002177165-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1195  
ID ABU67365 standard; protein; 299 AA.  
DE Human secreted protein PRO301.  
FN US2003023054-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1196  
ID ABU67160 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
FN US2003032062-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1197  
ID ABO14885 standard; protein; 299 AA.  
DE Human secreted / transmembrane polypeptide PRO301.  
FN US2003036060-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1198  
ID ABU07736 standard; protein; 299 AA.  
DE Human A-33 related antigen PRO301.  
FN US2002182206-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1199  
ID AAO16451 standard; protein; 299 AA.  
DE Human junctional adhesion molecule 1 (huJAM1).  
FN WO2003008541-A2.  
PD 30-JAN-2003.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1200  
ID ABU67028 standard; protein; 299 AA.  
DE Human secreted/transmembrane, PRO, protein SEQ ID 366.  
FN US2003032155-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1201

ID ABU69642 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003017463-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1202  
ID ABU79802 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein PRO301.  
PN US2003032057-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1203  
ID ABO14824 standard; protein; 299 AA.  
DE Human secreted / transmembrane polypeptide PRO301.  
PN US2003027143-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1204  
ID ADA45885 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003022328-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1205  
ID ADA76316 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003073212-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1206  
ID ADB29324 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003092002-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1207  
ID ADA18966 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003054517-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1208  
ID ADA61589 standard; protein; 299 AA.  
DE Homo sapiens.  
PN US2003049816-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1209  
ID ADB19374 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003068796-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1210  
ID ADB27915 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003082704-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1211  
ID ADA86394 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003082711-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1212  
ID ADB15958 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003087350-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1213  
ID ADA47744 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003073215-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1214  
ID ADA18180 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003039971-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1215  
ID ABO32776 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein PRO301.  
PN US2003045693-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1216  
ID ADA67539 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003068795-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1217  
ID ADB30546 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003068794-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1218  
ID ADA85842 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003082693-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 6; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1219  
ID ADA97054 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.

PN US2003082705-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.3%; Score 196; DB 6; Length 299;  
RESULT 1220  
ID ADA79358 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003082763-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.3%; Score 196; DB 6; Length 299;  
RESULT 1221  
ID ADA87497 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003087345-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.3%; Score 196; DB 6; Length 299;  
RESULT 1222  
ID ADB16699 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003087349-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.3%; Score 196; DB 6; Length 299;  
RESULT 1223  
ID ABO34836 standard; protein; 299 AA.  
DE Human PRO polypeptide #21.  
PN US2003044793-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.3%; Score 196; DB 6; Length 299;  
RESULT 1224  
ID ADA16155 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003049621-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.3%; Score 196; DB 6; Length 299;  
RESULT 1225  
ID ADA91791 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003082694-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.3%; Score 196; DB 6; Length 299;  
RESULT 1226  
ID ADB14854 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003087351-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.3%; Score 196; DB 6; Length 299;  
RESULT 1227  
ID ADA47263 standard; protein; 299 AA.  
DE Human secreted/transmembrane polypeptide PRO301.  
PN US2003044844-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.3%; Score 196; DB 6; Length 299;  
RESULT 1228  
ID ADB18815 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003073211-A1.

PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.3%; Score 196; DB 6; Length 299;  
RESULT 1229  
ID ADA94030 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003077722-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.3%; Score 196; DB 6; Length 299;  
RESULT 1230  
ID ADB19926 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003082691-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.3%; Score 196; DB 6; Length 299;  
RESULT 1231  
ID ADB13238 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003082710-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.3%; Score 196; DB 6; Length 299;  
RESULT 1232  
ID ABO43331 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003044945-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.3%; Score 196; DB 6; Length 299;  
RESULT 1233  
ID ADA74492 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003068798-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.3%; Score 196; DB 6; Length 299;  
RESULT 1234  
ID ADA42300 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003054401-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.3%; Score 196; DB 6; Length 299;  
RESULT 1235  
ID ADB24725 standard; protein; 299 AA.  
DE Human PRO polypeptide SEQ ID NO 366.  
PN US2003077713-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.3%; Score 196; DB 6; Length 299;  
RESULT 1236  
ID ADA82249 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003082701-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 10.3%; Score 196; DB 6; Length 299;  
RESULT 1237  
ID ADA75212 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003073216-A1.  
PD 17-APR-2003.

PA	(GETH ) GENENTECH INC.	Query Match	10.3%;	Score 196;	DB 6;	Length 299;
		Best Local Similarity	24.8%;	Pred. No. 3e-07;		
RESULT 1238						
ID	ADA85290 standard; protein; 299 AA.					
DE	Novel human secreted and transmembrane protein PRO301.					
PN	US2003082695-A1.					
PD	01-MAY-2003.					
PA	(GETH ) GENENTECH INC.	Query Match	10.3%;	Score 196;	DB 6;	Length 299;
		Best Local Similarity	24.8%;	Pred. No. 3e-07;		
RESULT 1239						
ID	ADA84738 standard; protein; 299 AA.					
DE	Novel human secreted and transmembrane protein PRO301.					
PN	US2003082708-A1.					
PD	01-MAY-2003.					
PA	(GETH ) GENENTECH INC.	Query Match	10.3%;	Score 196;	DB 6;	Length 299;
		Best Local Similarity	24.8%;	Pred. No. 3e-07;		
RESULT 1240						
ID	ABO17514 standard; protein; 299 AA.					
DE	Human PRO polypeptide #21.					
PN	US2003064367-A1.					
PD	03-APR-2003.					
PA	(GETH ) GENENTECH INC.	Query Match	10.3%;	Score 196;	DB 6;	Length 299;
		Best Local Similarity	24.8%;	Pred. No. 3e-07;		
RESULT 1241						
ID	ADB29994 standard; protein; 299 AA.					
DE	Human PRO polypeptide #183.					
PN	US2003073214-A1.					
PD	17-APR-2003.					
PA	(GETH ) GENENTECH INC.	Query Match	10.3%;	Score 196;	DB 6;	Length 299;
		Best Local Similarity	24.8%;	Pred. No. 3e-07;		
RESULT 1242						
ID	ADA80522 standard; protein; 299 AA.					
DE	Human PRO polypeptide #183.					
PN	US2003082761-A1.					
PD	01-MAY-2003.					
PA	(GETH ) GENENTECH INC.	Query Match	10.3%;	Score 196;	DB 6;	Length 299;
		Best Local Similarity	24.8%;	Pred. No. 3e-07;		
RESULT 1243						
ID	ADA75764 standard; protein; 299 AA.					
DE	Human PRO polypeptide #183.					
PN	US2003082703-A1.					
PD	01-MAY-2003.					
PA	(GETH ) GENENTECH INC.	Query Match	10.3%;	Score 196;	DB 6;	Length 299;
		Best Local Similarity	24.8%;	Pred. No. 3e-07;		
RESULT 1244						
ID	ADA46989 standard; protein; 299 AA.					
DE	Human PRO polypeptide #183.					
PN	US2003073210-A1.					
PD	17-APR-2003.					
PA	(GETH ) GENENTECH INC.	Query Match	10.3%;	Score 196;	DB 6;	Length 299;
		Best Local Similarity	24.8%;	Pred. No. 3e-07;		
RESULT 1245						
ID	ADB25285 standard; protein; 299 AA.					
DE	Human PRO polypeptide SEQ ID NO 366.					
PN	US2003077715-A1.					
PD	24-APR-2003.					
PA	(GETH ) GENENTECH INC.	Query Match	10.3%;	Score 196;	DB 6;	Length 299;
		Best Local Similarity	24.8%;	Pred. No. 3e-07;		
RESULT 1246						
ID	ADA93461 standard; protein; 299 AA.					
DE	Human PRO polypeptide #183.					
PN	US2003077721-A1.					
PD	24-APR-2003.					
PA	(GETH ) GENENTECH INC.	Query Match	10.3%;	Score 196;	DB 6;	Length 299;
		Best Local Similarity	24.8%;	Pred. No. 3e-07;		
RESULT 1247						
ID	ADB26811 standard; protein; 299 AA.					
DE	Human PRO polypeptide #183.					
PN	US2003092147-A1.					
PD	15-MAY-2003.					
PA	(GETH ) GENENTECH INC.	Query Match	10.3%;	Score 196;	DB 6;	Length 299;
		Best Local Similarity	24.8%;	Pred. No. 3e-07;		
RESULT 1248						
ID	ADB31098 standard; protein; 299 AA.					
DE	Human PRO polypeptide #183.					
PN	US2003096386-A1.					
PD	22-MAY-2003.					
PA	(GETH ) GENENTECH INC.	Query Match	10.3%;	Score 196;	DB 6;	Length 299;
		Best Local Similarity	24.8%;	Pred. No. 3e-07;		

Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1256  
ID ADA77523 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003068797-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1257  
ID ADB18263 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003077710-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1258  
ID ADA86946 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003082709-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1259  
ID ADA16579 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003039969-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1260  
ID ADA13008 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003049622-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1261  
ID ADA41876 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003082540-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1262  
ID ADA8049 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003082700-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1263  
ID ADA46437 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003054516-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1264  
ID ADA17223 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003017498-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;

RESULT 1265  
ID ADA42726 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003054351-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1266  
ID ADB28467 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003082699-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1267  
ID ADB29019 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003082706-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1268  
ID ADA76971 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003059909-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1269  
ID ADA88601 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003073213-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1270  
ID ADA97606 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003082686-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1271  
ID ADB27363 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003022239-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1272  
ID ADB22296 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003087344-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1273  
ID ABO19860 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein PRO302.  
PN US2003044902-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1274  
ID ABO1575 standard; protein; 299 AA.  
DE Human PRO polypeptide #21.

PN US2003064923-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1275  
ID ADA66987 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003068793-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1276  
ID ADB22848 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003077711-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1277  
ID ADB23621 standard; protein; 299 AA.  
DE Human PRO polypeptide SEQ ID NO 366.  
PN US2003077712-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1278  
ID ADA92343 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003082712-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1279  
ID ADB15406 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003087352-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1280  
ID ADB38658 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003082766-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1281  
ID ADB38106 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003087347-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1282  
ID ADB66578 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003082689-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1283  
ID ADB89658 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003082698-A1.

PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1284  
ID ADB90390 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003082762-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1285  
ID ADB77645 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003077654-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1286  
ID ADB39491 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003082764-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1287  
ID ADB74781 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003082542-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1288  
ID ADB47114 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003082687-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1289  
ID ADB86721 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003082697-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1290  
ID ADB77326 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003082696-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1291  
ID ADB34483 standard; protein; 299 AA.  
DE Human PRO polypeptide SEQ ID NO 366.  
PN US2003077717-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1292  
ID ADB35587 standard; protein; 299 AA.  
DE Human PRO polypeptide SEQ ID NO 366.  
PN US2003077719-A1.  
PD 24-APR-2003.



PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1293  
ID ADB33931 standard; protein; 299 AA.  
DE Human PRO polypeptide SEQ ID NO 366.  
PN US2003077716-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1294  
ID ADB35035 standard; protein; 299 AA.  
DE Human PRO polypeptide SEQ ID NO 366.  
PN US2003077718-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1295  
ID ADB36139 standard; protein; 299 AA.  
DE Human PRO polypeptide SEQ ID NO 366.  
PN US2003077720-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1296  
ID ADB46534 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003082692-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1297  
ID ADC28427 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003059772-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1298  
ID ADC39627 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003059828-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1299  
ID ADC40141 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003059829-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1300  
ID ADC18969 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003036061-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1301  
ID ADC34265 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003036094-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.

Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1302  
ID ADC29320 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003049676-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1303  
ID ADC28851 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003049677-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1304  
ID ADC40736 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003054400-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1305  
ID ADC19393 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003054441-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1306  
ID ADC33841 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003073077-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1307  
ID ADC12911 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003073079-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1308  
ID ADC50407 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003092106-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1309  
ID ADC71954 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003092107-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1310  
ID ADC59933 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003092105-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1311  
ID ADC34265 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003036094-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1311  
ID ADC52940 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein Seq ID366.  
PN US2003087365-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1312  
ID ADC57294 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein Seq ID366.  
PN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1313  
ID ADC60485 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1314  
ID ADC50960 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003087361-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1315  
ID ADC65487 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003087362-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1316  
ID ADC54585 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein Seq ID366.  
PN US2003087363-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1317  
ID ADC53546 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein Seq ID366.  
PN US2003087364-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1318  
ID ADC59069 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein Seq ID366.  
PN US2003087359-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1319  
ID ADC55947 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein Seq ID366.  
PN US2003087360-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1320  
ID ADC58517 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein Seq ID366.  
PN US2003087346-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1321  
ID ADC13363 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003082541-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1322  
ID ADD03191 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003092104-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1323  
ID ADC90183 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003087348-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1324  
ID ADC69602 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003194770-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1325  
ID ADC48491 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003194773-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1326  
ID ADD10020 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003194776-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1327  
ID ADD04595 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003087354-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1328  
ID ADC80551 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003092103-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1329

ID ADD11058 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
FN US2003194774-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1330  
ID ADD10343 standard; protein; 299 AA.  
DE Human secreted/transmembrane PRO polypeptide #27.  
FN US2003105011-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1331  
ID ADC47939 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
FN US2003194771-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1332  
ID ADD04918 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
FN US2003104469-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1333  
ID ADC79999 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
FN US2003087358-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1334  
ID ADD11303 standard; protein; 299 AA.  
DE Human secreted/transmembrane PRO polypeptide #27.  
FN US2003105013-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1335  
ID ADD09468 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
FN US2003194775-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1336  
ID ADD03924 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
FN US2003104381-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1337  
ID ADD03500 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
FN US2003108983-A1.  
PD 12-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1338  
ID ADD41181 standard; protein; 299 AA.

DE Novel human secreted and transmembrane protein PRO301.  
FN US2003203438-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1339  
ID ADD52320 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
FN US2003194769-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1340  
ID ADD53060 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
FN US2003194792-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1341  
ID ADD53612 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
FN US2003203437-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1342  
ID ADD37096 standard; protein; 299 AA.  
DE Human secreted/transmembrane PRO polypeptide #27.  
FN US2003105012-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1343  
ID ADD51768 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
FN US2003194779-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1344  
ID ADD02567 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
FN US2003203431-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1345  
ID ADD02001 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
FN US2003203430-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1346  
ID ADD54183 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
FN US2003203432-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1347  
ID ADD92500 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.

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PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1348
ID ADD91396 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1349
ID ADE04010 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1350
ID ADE32307 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1351
ID ADE22239 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1352
ID ADD79463 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1353
ID ADE41999 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1354
ID ADE17816 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1355
ID ADD91948 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1356
ID ADE33411 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194767-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1357
ID ADE33963 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1358
ID ADD80015 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207417-A1.
PD 08-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1359
ID ADD93052 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1360
ID ADE19472 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1361
ID ADE34752 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1362
ID ADE18920 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1363
ID ADE43116 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1364
ID ADD95905 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 7; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1365
ID ADE22791 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199064-A1.
PD 23-OCT-2003.
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PA (GETH ) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1366
ID AD078909 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1367
ID ADE32859 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
FN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1368
ID ADE42551 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1369
ID ADD80567 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1370
ID ADD89595 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1371
ID ADE40879 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1372
ID ADE04678 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1373
ID ADE92807 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1374
ID ADG21516 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
FN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1375
ID ADG23157 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
FN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1376
ID ADE97492 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1377
ID ADG80556 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1378
ID ADG80004 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
FN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1379
ID ADG63772 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
FN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1380
ID ADH62528 standard; protein; 299 AA.
DE Human PRO301 protein.
FN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1381
ID ADH59235 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
FN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1382
ID ADH55296 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
FN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.3%; Score 196; DB 7; Length 299;
Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1383

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ID ADH5848 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003207379-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1384  
ID ADI38014 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003054352-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1385  
ID ADI64067 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003207385-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1386  
ID ADI65016 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003207386-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1387  
ID ADI63515 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003207387-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1388  
ID ADH81929 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003207388-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1389  
ID ADH81377 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003207377-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1390  
ID ADJ26282 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003054349-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1391  
ID ADM82546 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003087355-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1392  
ID ADN15945 standard; protein; 299 AA.

DE Novel human secreted and transmembrane protein PRO301.  
PN US2003087353-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1393  
ID ADN16574 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003087385-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1394  
ID ADN15393 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003087356-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1395  
ID ADN14841 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003087357-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 7; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1396  
ID ADC81103 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003092115-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1397  
ID ADE79197 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003135025-A1.  
PD 17-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1398  
ID ADD76551 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003100087-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1399  
ID ADD87915 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003092113-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1400  
ID ADD86319 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003203440-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1401  
ID ADE79621 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.

PN US2003130489-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1402 standard; protein; 299 AA.  
ID ADE75767 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003211571-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1403 standard; protein; 299 AA.  
ID ADE73297 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003129592-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1404 standard; protein; 299 AA.  
ID ADE41304 standard; protein; 299 AA.  
DE Human secreted/transmembrane PRO polypeptide #27.  
PN US2003100497-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1405 standard; protein; 299 AA.  
ID ADE23343 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003092108-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1406 standard; protein; 299 AA.  
ID ADE23895 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003092110-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1407 standard; protein; 299 AA.  
ID ADE24538 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003092111-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1408 standard; protein; 299 AA.  
ID ADD87363 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003203439-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1409 standard; protein; 299 AA.  
ID ADE89229 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003199062-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1410 standard; protein; 299 AA.  
ID ADE41186 standard; protein; 299 AA.  
DE Human secreted/transmembrane polypeptide PRO301.  
PN US2003104558-A1.

PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1411 standard; protein; 299 AA.  
ID ADE73832 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003148370-A1.  
PD 07-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1412 standard; protein; 299 AA.  
ID ADE18368 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003194794-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1413 standard; protein; 299 AA.  
ID ADE88677 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003199054-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1414 standard; protein; 299 AA.  
ID ADE93386 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003211576-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1415 standard; protein; 299 AA.  
ID ADE94697 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003199027-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1416 standard; protein; 299 AA.  
ID ADE91108 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003199061-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1417 standard; protein; 299 AA.  
ID ADE95249 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003199052-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1418 standard; protein; 299 AA.  
ID ADE93359 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003199060-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1419 standard; protein; 299 AA.  
ID ADF34940 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003199029-A1.  
PD 23-OCT-2003.

PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1420  
ID ADE98505 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003211569-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1421  
ID ADE92255 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003199051-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1422  
ID ADE90556 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003199063-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1423  
ID ADE91703 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003199058-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1424  
ID ADE98932 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003211568-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1425  
ID ADG40402 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003225253-A1.  
PD 04-DEC-2003.  
PA (DESN/) DESNOYERS L.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P. J.  
PA (GURN/) GURNEY A. L.  
PA (MATH/) MATHER J. P.  
PA (WILL/) WILLIAMS P. M.  
PA (WOOD/) WOOD W. I.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1426  
ID ADF73796 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003180312-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1427  
ID ADG02282 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003207352-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;

RESULT 1428  
ID ADG22068 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003207360-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1429  
ID ADG20138 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003207376-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1430  
ID ADF98044 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003207422-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1431  
ID ADG24261 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003207426-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1432  
ID ADF98615 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003208055-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1433  
ID ADG03446 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003207351-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1434  
ID ADF99167 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003207353-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1435  
ID ADG16752 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003207359-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1436  
ID ADG05211 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003207375-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1437  
ID ADG05211 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003207375-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;



ID ADG19478 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003207425-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1438  
ID ADF73372 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003166051-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1439  
ID ADG13315 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003207357-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1440  
ID ADG08372 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003207424-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1441  
ID ADG15542 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003219885-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1442  
ID ADF96940 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003207371-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1443  
ID ADG06125 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003207374-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1444  
ID ADG23709 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003207389-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1445  
ID ADG03398 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003207423-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1446  
ID ADG24899 standard; protein; 299 AA.

DE Novel human secreted and transmembrane protein PRO301.  
PN US2003207427-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1447  
ID ADG07196 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003207350-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1448  
ID ADG07748 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003207356-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1449  
ID ADG55243 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003194778-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1450  
ID ADG60907 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003207390-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1451  
ID ADG62011 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003207428-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1452  
ID ADG92215 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003027145-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1453  
ID ADG82212 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003207358-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1454  
ID ADG57451 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003207362-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1455  
ID ADG56899 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.

PN US2003207364-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1456  
ID ADG55795 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003207365-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1457  
ID ADG58555 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003207368-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1458  
ID ADG70921 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003207420-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1459  
ID ADG92642 standard; protein; 299 AA.  
DE Human secreted/transmembrane protein, #25.  
PN US2003027146-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1460  
ID ADG58003 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003207363-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1461  
ID ADG53587 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003207415-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1462  
ID ADG71473 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003207421-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1463  
ID ADG81660 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003207805-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1464  
ID ADH30622 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003077723-A1.  
PD 24-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1465  
ID ADG63621 standard; protein; 299 AA.  
DE Human secreted/transmembrane polypeptide PRO301.  
PN US2003180796-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1466  
ID ADH11989 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003207419-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1467  
ID ADG52411 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003207414-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1468  
ID ADG54139 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003207416-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1469  
ID ADG81108 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003194793-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1470  
ID ADG56347 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003207366-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1471  
ID ADH12613 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003207378-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1472  
ID ADG61459 standard; protein; 299 AA.  
DE Novel human secreted and transmembrane protein PRO301.  
PN US2003207429-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.3%; Score 196; DB 8; Length 299;  
Best Local Similarity 24.8%; Pred. No. 3e-07;  
RESULT 1473  
ID ADH28546 standard; protein; 299 AA.  
DE Human PRO polypeptide #183.  
PN US2003022331-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.

Query Match 10.3%; Score 196; DB 8; Length 299;  
 Best Local Similarity 24.8%; Pred. No. 3e-07;  
 RESULT 1474  
 ID ADG54691 standard; protein; 299 AA.  
 DE Novel human secreted and transmembrane protein PRO301.  
 PN US2003207367-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.3%; Score 196; DB 8; Length 299;  
 Best Local Similarity 24.8%; Pred. No. 3e-07;  
 RESULT 1475  
 ID ADG59731 standard; protein; 299 AA.  
 DE Novel human secreted and transmembrane protein PRO301.  
 PN US2003207369-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.3%; Score 196; DB 8; Length 299;  
 Best Local Similarity 24.8%; Pred. No. 3e-07;  
 RESULT 1476  
 ID ADH20431 standard; protein; 299 AA.  
 DE Human secreted/transmembrane protein, #25.  
 PN US2004005553-A1.  
 PD 08-JAN-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.3%; Score 196; DB 8; Length 299;  
 Best Local Similarity 24.8%; Pred. No. 3e-07;  
 RESULT 1477  
 ID ADH43487 standard; protein; 299 AA.  
 DE Human PRO polypeptide #27.  
 PN US2003224984-A1.  
 PD 04-DEC-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.3%; Score 196; DB 8; Length 299;  
 Best Local Similarity 24.8%; Pred. No. 3e-07;  
 RESULT 1478  
 ID ADH07286 standard; protein; 299 AA.  
 DE Human secreted/transmembrane protein, #25.  
 PN US2004006211-A1.  
 PD 08-JAN-2004.  
 PA (DESN/) DESNOYERS L.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GURN/) GURNEY A L.  
 PA (MATH/) MATHER J P.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 Query Match 10.3%; Score 196; DB 8; Length 299;  
 Best Local Similarity 24.8%; Pred. No. 3e-07;  
 RESULT 1479  
 ID ADH59831 standard; protein; 299 AA.  
 DE Human secreted/transmembrane protein, #25.  
 PN US2003215904-A1.  
 PD 20-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.3%; Score 196; DB 8; Length 299;  
 Best Local Similarity 24.8%; Pred. No. 3e-07;  
 RESULT 1480  
 ID ADH06859 standard; protein; 299 AA.  
 DE Human secreted/transmembrane protein, #25.  
 PN US2004005665-A1.  
 PD 08-JAN-2004.  
 PA (DESN/) DESNOYERS L.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GURN/) GURNEY A L.  
 PA (MATH/) MATHER J P.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 Query Match 10.3%; Score 196; DB 8; Length 299;  
 Best Local Similarity 24.8%; Pred. No. 3e-07;  
 RESULT 1481  
 ID ADH11155 standard; protein; 299 AA.  
 DE Human PRO polypeptide #183.

PN US2003207361-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.3%; Score 196; DB 8; Length 299;  
 Best Local Similarity 24.8%; Pred. No. 3e-07;  
 RESULT 1482  
 ID ADI18601 standard; protein; 299 AA.  
 DE Human secreted/transmembrane protein, #25.  
 PN US2003152999-A1.  
 PD 14-AUG-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.3%; Score 196; DB 8; Length 299;  
 Best Local Similarity 24.8%; Pred. No. 3e-07;  
 RESULT 1483  
 ID ADI65321 standard; protein; 299 AA.  
 DE Human secreted/transmembrane protein, #25.  
 PN US2003148419-A1.  
 PD 07-AUG-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.3%; Score 196; DB 8; Length 299;  
 Best Local Similarity 24.8%; Pred. No. 3e-07;  
 RESULT 1484  
 ID ADI37584 standard; protein; 299 AA.  
 DE Human secreted/transmembrane protein, #25.  
 PN US2003096340-A1.  
 PD 22-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.3%; Score 196; DB 8; Length 299;  
 Best Local Similarity 24.8%; Pred. No. 3e-07;  
 RESULT 1485  
 ID ADG09898 standard; protein; 299 AA.  
 DE Novel human secreted and transmembrane protein PRO301.  
 PN US2004009548-A1.  
 PD 15-JAN-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.3%; Score 196; DB 8; Length 299;  
 Best Local Similarity 24.8%; Pred. No. 3e-07;  
 RESULT 1486  
 ID ADH97380 standard; protein; 299 AA.  
 DE Human secreted/transmembrane protein, #25.  
 PN US2003190610-A1.  
 PD 09-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.3%; Score 196; DB 8; Length 299;  
 Best Local Similarity 24.8%; Pred. No. 3e-07;  
 RESULT 1487  
 ID ADI15369 standard; protein; 299 AA.  
 DE Novel human secreted and transmembrane protein PRO301.  
 PN US2003207382-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.3%; Score 196; DB 8; Length 299;  
 Best Local Similarity 24.8%; Pred. No. 3e-07;  
 RESULT 1488  
 ID ADG09246 standard; protein; 299 AA.  
 DE Novel human secreted and transmembrane protein PRO301.  
 PN US2004009547-A1.  
 PD 15-JAN-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.3%; Score 196; DB 8; Length 299;  
 Best Local Similarity 24.8%; Pred. No. 3e-07;  
 RESULT 1489  
 ID ADI65748 standard; protein; 299 AA.  
 DE Human secreted/transmembrane protein, #25.  
 PN US2003148371-A1.  
 PD 07-AUG-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.3%; Score 196; DB 8; Length 299;  
 Best Local Similarity 24.8%; Pred. No. 3e-07;  
 RESULT 1490  
 ID ADI14701 standard; protein; 299 AA.  
 DE Novel human secreted and transmembrane protein PRO301.  
 PN US2003207383-A1.

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PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 8; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1491
ID ADH60491 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
  Query Match 10.3%; Score 196; DB 8; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1492
ID ADI18296 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 8; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1493
ID ADJ99548 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 8; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1494
ID ADL08741 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 8; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1495
ID ADI47176 standard; protein; 299 AA.
DE Human JAM-1 protein sequence.
PN WO2004003145-A2.
PD 08-JAN-2004.
PA (NAST-) NASTECH PHARM CO INC.
  Query Match 10.3%; Score 196; DB 8; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1496
ID ADM25082 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 8; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1497
ID ADK40844 standard; protein; 299 AA.
DE Human platelet F11 receptor #1.
PN US6695688-B1.
PD 02-MAR-2004.
PA (UINY ) UNIV NEW YORK STATE RES FOUND.
  Query Match 10.3%; Score 196; DB 8; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1498
ID ADJ63577 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 8; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1499
ID ADM29832 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.3%; Score 196; DB 8; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;
RESULT 1500
ID ADQ95890 standard; protein; 299 AA.
DE T cell activation associated protein #34.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASahi KASEI PHARMA CORP.
  Query Match 10.3%; Score 196; DB 8; Length 299;
  Best Local Similarity 24.8%; Pred. No. 3e-07;

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OM protein - protein search, using sw model

Run on: May 5, 2005, 07:52:29 ; Search time 44 Seconds  
(without alignments)  
632.820 Million cell updates/sec

Title: US-09-978-375A-59

Perfect score: 1908

Sequence: 1 MSLLLLLLVYVGLGTH.....TKAETTPSMIPQSRAFQTV 373

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1162	60.9	894	4	US-09-949-016-10605
2	471	24.7	365	4	US-09-899-634C-4
3	467	24.5	365	3	US-08-928-383B-2
4	465	24.4	365	2	US-08-979-424-3
5	465	24.4	365	3	US-09-272-496-2
6	465	24.4	365	4	US-09-949-016-6064
7	465	24.4	383	4	US-09-949-016-11050
8	458.5	24.0	365	3	US-08-928-383B-23
9	457.5	24.0	365	3	US-08-928-383B-26
10	446.5	23.4	365	3	US-08-928-383B-24
11	378.5	17.8	261	4	US-09-899-634C-2
12	340.5	19.8	466	4	US-09-604-107A-8
13	321	16.8	365	4	US-09-336-536-40
14	321	16.8	394	4	US-09-336-536-39
15	308.5	16.2	319	1	US-08-597-495B-22
16	308.5	16.2	319	3	US-09-068-051A-22
17	308.5	16.2	319	4	US-09-336-536-67
18	308.5	16.2	319	4	US-09-254-465A-6
19	308.5	16.2	319	4	US-09-953-499-6
20	308	16.1	316	4	US-09-953-499-13
21	307.5	16.1	390	2	US-08-979-424-1
22	307.5	16.1	390	4	US-09-907-794A-39
23	307.5	16.1	390	4	US-09-905-125A-39
24	307.5	16.1	390	4	US-09-902-775A-39
25	307.5	16.1	390	4	US-09-906-700-39
26	307.5	16.1	390	4	US-09-903-603A-39
27	307.5	16.1	390	4	US-09-904-920A-39
28	307.5	16.1	390	4	US-09-909-064-39
29	307.5	16.1	390	4	US-09-905-381A-39
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87	307.5	16.1	390	4	US-09-963-11050
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94	307.5	16.1	390	4	US-09-970-11050
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97	307.5	16.1	390	4	US-09-973-11050
98	307.5	16.1	390	4	US-09-974-11050
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Sequence 64, Appl

101	163.5	8.6	312	4	US-09-906-700-64	Sequence 64, Appl	174	141.5	7.4	316	4	US-09-910-174B-24	Sequence 24, Appl
102	163.5	8.6	312	4	US-09-903-603A-64	Sequence 64, Appl	175	141.5	7.4	316	4	US-09-620-461-24	Sequence 24, Appl
103	163.5	8.6	312	4	US-09-904-920A-64	Sequence 64, Appl	176	141.5	7.4	342	2	US-08-724-394B-6	Sequence 6, Appl
104	163.5	8.6	312	4	US-09-909-064-64	Sequence 64, Appl	177	141	7.4	527	4	US-09-910-174B-10	Sequence 10, Appl
105	163.5	8.6	312	4	US-09-905-381A-64	Sequence 64, Appl	178	141	7.4	527	4	US-09-620-461-10	Sequence 10, Appl
106	163.5	8.6	312	4	US-09-906-618-64	Sequence 64, Appl	179	137.5	7.2	540	2	US-08-724-394A-4	Sequence 4, Appl
107	163.5	8.6	312	4	US-09-953-499-9	Sequence 9, Appl	180	137	7.2	802	3	US-09-173-151A-33	Sequence 33, Appl
108	163.5	8.6	439	3	US-09-383-586-32	Sequence 32, Appl	181	136.5	7.2	350	4	US-09-651-200-25	Sequence 25, Appl
109	163.5	8.6	439	3	US-08-823-038A-32	Sequence 32, Appl	182	136.5	7.2	350	4	US-09-910-174B-17	Sequence 17, Appl
110	162	8.5	584	4	US-09-910-174B-16	Sequence 16, Appl	183	136.5	7.2	350	4	US-09-620-461-17	Sequence 17, Appl
111	162	8.5	584	4	US-09-620-461-16	Sequence 16, Appl	184	135.5	7.1	514	4	US-09-949-016-11380	Sequence 11380, A
112	158	8.3	394	4	US-08-855-323-17	Sequence 17, Appl	185	135.5	7.1	517	4	US-09-723-368-4	Sequence 4, Appl
113	156	8.2	394	4	US-09-656-952-20	Sequence 20, Appl	186	135.5	7.1	1070	4	US-09-961-403-3	Sequence 3, Appl
114	156	8.2	1059	4	US-09-907-794A-290	Sequence 290, App	187	135	7.1	290	4	US-09-910-174B-19	Sequence 19, Appl
115	156	8.2	1059	4	US-09-905-125A-290	Sequence 290, App	188	135	7.1	290	4	US-09-620-461-19	Sequence 19, Appl
116	156	8.2	1059	4	US-09-902-775A-290	Sequence 290, App	189	135	7.1	518	4	US-09-919-172-20	Sequence 20, Appl
117	156	8.2	1059	4	US-09-906-700-290	Sequence 290, App	190	135	7.1	581	2	US-08-724-394A-3	Sequence 3, Appl
118	156	8.2	1059	4	US-09-903-603A-290	Sequence 290, App	191	135	7.1	590	3	US-09-310-463-22	Sequence 22, Appl
119	156	8.2	1059	4	US-09-904-920A-290	Sequence 290, App	192	135	7.1	590	4	US-08-842-248A-22	Sequence 22, Appl
120	156	8.2	1059	4	US-09-909-064-290	Sequence 290, App	193	135	7.1	837	4	US-09-949-016-6515	Sequence 6515, Ap
121	156	8.2	1059	4	US-09-905-381A-290	Sequence 290, App	194	134.5	7.0	738	6	5264554-2	Patent No. 5264554
122	156	8.2	1059	4	US-09-906-618-290	Sequence 290, App	195	134.5	7.0	738	6	5264554-2	Patent No. 5264554
123	156	8.2	1119	4	US-09-907-794A-294	Sequence 294, App	196	134.5	7.0	1091	3	US-08-986-485-5	Sequence 5, Appl
124	156	8.2	1119	4	US-09-905-125A-294	Sequence 294, App	197	134	7.0	529	4	US-09-910-174B-13	Sequence 13, Appl
125	156	8.2	1119	4	US-09-902-775A-294	Sequence 294, App	198	134	7.0	529	4	US-09-620-461-13	Sequence 13, Appl
126	156	8.2	1119	4	US-09-906-700-294	Sequence 294, App	199	133.5	7.0	182	3	US-09-724-864-50	Sequence 50, Appl
127	156	8.2	1119	4	US-09-903-603A-294	Sequence 294, App	200	133	7.0	1248	4	US-09-949-016-10595	Sequence 10595, A
128	156	8.2	1119	4	US-09-904-920A-294	Sequence 294, App	201	133	7.0	1248	4	US-09-949-016-10596	Sequence 10596, A
129	156	8.2	1119	4	US-09-909-064-294	Sequence 294, App	202	133	7.0	1297	3	US-09-540-245A-17	Sequence 17, Appl
130	156	8.2	1119	4	US-09-905-381A-294	Sequence 294, App	203	133	7.0	1311	1	US-08-340-011-5	Sequence 5, Appl
131	156	8.2	1119	4	US-09-906-618-294	Sequence 294, App	204	133	7.0	1311	3	US-08-901-710-5	Sequence 5, Appl
132	155	8.1	313	4	US-09-700-397-3	Sequence 4, Appl	205	133	7.0	1311	4	US-09-169-079-5	Sequence 5, Appl
133	155	8.1	344	4	US-09-700-397-3	Sequence 3, Appl	206	132	6.9	286	4	US-09-667-135-36	Sequence 36, Appl
134	153.5	8.0	321	4	US-09-254-465A-2	Sequence 2, Appl	207	131.5	6.9	581	2	US-08-724-394A-2	Sequence 2, Appl
135	153.5	8.0	321	4	US-09-953-499-2	Sequence 2, Appl	208	131	6.9	288	4	US-09-651-200-14	Sequence 14, Appl
136	152.5	8.0	526	4	US-09-910-174B-9	Sequence 9, Appl	209	131	6.9	450	4	US-09-907-794A-320	Sequence 320, App
137	152.5	8.0	526	4	US-09-620-461-9	Sequence 9, Appl	210	131	6.9	450	4	US-09-905-125A-320	Sequence 320, App
138	152.5	8.0	526	4	US-09-949-016-6122	Sequence 6122, Ap	211	131	6.9	450	4	US-09-902-775A-320	Sequence 320, App
139	152.5	8.0	540	4	US-09-949-016-11644	Sequence 11644, A	212	131	6.9	450	4	US-09-906-700-320	Sequence 320, App
140	151.5	7.9	95	3	US-08-928-383B-11	Sequence 17, Appl	213	131	6.9	450	4	US-09-903-603A-320	Sequence 320, App
141	151.5	7.9	1101	3	US-08-986-485-2	Sequence 2, Appl	214	131	6.9	450	4	US-09-904-920A-320	Sequence 320, App
142	151	7.9	501	2	US-08-408-095-31	Sequence 31, Appl	215	131	6.9	450	4	US-09-909-064-320	Sequence 320, App
143	150	7.9	205	3	US-09-462-270-4	Sequence 4, Appl	216	131	6.9	450	4	US-09-905-381A-320	Sequence 320, App
144	150	7.9	319	4	US-09-910-174B-12	Sequence 12, Appl	217	131	6.9	450	4	US-09-906-618-320	Sequence 320, App
145	150	7.9	319	4	US-09-620-461-12	Sequence 12, Appl	218	131	6.9	4391	4	US-10-006-011A-2	Sequence 2, Appl
146	150	7.9	357	4	US-09-910-174B-14	Sequence 14, Appl	219	130.5	6.8	458	4	US-09-435-956A-1	Sequence 1, Appl
147	150	7.9	357	4	US-09-620-461-14	Sequence 14, Appl	220	130	6.8	588	4	US-09-949-016-10547	Sequence 10547, A
148	150	7.9	513	4	US-09-910-174B-18	Sequence 18, Appl	221	129	6.8	1338	3	US-08-750-141A-3	Sequence 3, Appl
149	150	7.9	513	4	US-09-620-461-18	Sequence 18, Appl	222	129	6.8	1338	4	US-09-119-014D-6	Sequence 6, Appl
150	149	7.8	318	4	US-09-656-952-2	Sequence 2, Appl	223	128.5	6.7	646	4	US-09-949-016-7344	Sequence 7344, Ap
151	148.5	7.8	610	2	US-08-724-394A-5	Sequence 5, Appl	224	128	6.7	615	2	US-08-752-307B-9	Sequence 9, Appl
152	148.5	7.8	738	3	US-08-478-208-32	Sequence 32, Appl	225	128	6.7	615	3	US-09-707-802-9	Sequence 9, Appl
153	148.5	7.8	738	4	US-09-336-536-73	Sequence 73, Appl	226	128	6.7	615	3	US-09-991-326-9	Sequence 9, Appl
154	147.5	7.7	315	4	US-09-910-174B-28	Sequence 28, Appl	227	128	6.7	819	4	US-09-949-016-11044	Sequence 11044, A
155	147.5	7.7	315	4	US-09-620-461-28	Sequence 28, Appl	228	128	6.7	1501	2	US-08-447-464-3	Sequence 3, Appl
156	147	7.7	344	4	US-09-656-952-19	Sequence 19, Appl	229	128	6.7	1501	2	US-08-716-679-3	Sequence 3, Appl
157	146.5	7.7	404	4	US-09-638-649-3	Sequence 3, Appl	230	127.5	6.7	288	2	US-08-147-772-2	Sequence 2, Appl
158	146.5	7.7	404	4	US-09-949-016-11025	Sequence 11025, A	231	127.5	6.7	288	2	US-08-456-104-6	Sequence 6, Appl
159	146.5	7.7	404	4	US-09-638-648-3	Sequence 3, Appl	232	127.5	6.7	288	2	US-08-101-624-23	Sequence 23, Appl
160	145	7.6	193	4	US-09-397-243D-4	Sequence 4, Appl	233	127.5	6.7	288	2	US-08-751-767A-6	Sequence 6, Appl
161	143.5	7.5	731	4	US-09-910-174B-15	Sequence 15, Appl	234	127.5	6.7	288	3	US-08-153-262-2	Sequence 2, Appl
162	143.5	7.5	731	4	US-09-620-461-15	Sequence 15, Appl	235	127.5	6.7	288	3	US-08-479-744A-29	Sequence 29, Appl
163	143	7.5	405	4	US-08-755-235-4	Sequence 4, Appl	236	127.5	6.7	288	3	US-08-280-757B-29	Sequence 29, Appl
164	143	7.5	523	4	US-09-910-174B-11	Sequence 11, Appl	237	127.5	6.7	288	3	US-09-159-135-2	Sequence 2, Appl
165	143	7.5	523	4	US-09-620-461-11	Sequence 11, Appl	238	127.5	6.7	288	3	US-08-205-697A-19	Sequence 19, Appl
166	143	7.5	816	4	US-09-949-016-10904	Sequence 10904, A	239	127.5	6.7	288	3	US-08-702-525-19	Sequence 19, Appl
167	142.5	7.5	340	4	US-09-651-200-2	Sequence 2, Appl	240	127.5	6.7	288	3	US-09-450-798-2	Sequence 2, Appl
168	142.5	7.5	441	4	US-09-651-200-4	Sequence 4, Appl	241	127.5	6.7	288	3	US-08-403-253A-2	Sequence 2, Appl
169	142.5	7.5	534	4	US-09-651-200-6	Sequence 6, Appl	242	127.5	6.7	288	4	US-09-651-200-13	Sequence 13, Appl
170	142.5	7.5	534	4	US-09-651-200-24	Sequence 24, Appl	243	127.5	6.7	288	4	US-09-667-135-34	Sequence 34, Appl
171	142	7.4	329	4	US-09-651-200-19	Sequence 19, Appl	244	127.5	6.7	288	4	US-08-435-816A-2	Sequence 2, Appl
172	142	7.4	504	4	US-09-949-016-7020	Sequence 7020, Ap	245	127.5	6.7	288	4	US-09-425-762-29	Sequence 29, Appl
173	142	7.4	511	4	US-09-949-016-10054	Sequence 10054, A	246	127.5	6.7	288	4	US-09-837-867A-19	Sequence 19, Appl

247	127.5	6.7	288	4	US-09-910-174B-5	Sequence 5, Appli	320	6.3	698	2	US-08-602-725-36	Sequence 36, Appl
248	127.5	6.7	288	4	US-09-620-461-5	Sequence 5, Appli	321	6.3	702	4	US-09-949-016-6484	Sequence 6484, Ap
249	127.5	6.7	288	4	US-08-453-386A-2	Sequence 2, Appli	322	6.3	734	2	US-08-389-459A-17	Sequence 17, Appl
250	127.5	6.7	288	4	US-09-206-132-6	Sequence 6, Appli	323	6.3	734	3	US-08-987-867A-17	Sequence 17, Appl
251	127.5	6.7	288	4	US-09-425-516-29	Sequence 29, Appl	324	6.3	740	4	US-09-949-016-8168	Sequence 8168, Ap
252	127.5	6.7	288	5	PCT-US95-02576-19	Sequence 19, Appl	325	6.3	795	4	US-09-949-016-7119	Sequence 7119, Ap
253	127.5	6.7	288	4	US-09-778-510-6	Sequence 6, Appli	326	6.3	806	3	US-09-383-630-3	Sequence 3, Appli
254	127.5	6.7	398	4	US-09-907-794A-84	Sequence 84, Appl	327	6.3	1953	4	US-09-917-254-92	Sequence 92, Appl
255	127.5	6.7	398	4	US-09-905-125A-84	Sequence 84, Appl	328	119.5	631	3	US-09-414-453A-12	Sequence 12, Appl
256	127.5	6.7	398	4	US-09-902-775A-84	Sequence 84, Appl	329	119.5	631	3	US-09-414-453A-12	Sequence 12, Appl
257	127.5	6.7	398	4	US-09-906-700-84	Sequence 84, Appl	330	119.5	631	3	US-09-310-463-20	Sequence 20, Appl
258	127.5	6.7	398	4	US-09-903-603A-84	Sequence 84, Appl	331	119.5	631	3	US-08-842-248A-20	Sequence 20, Appl
259	127.5	6.7	398	4	US-09-904-920A-84	Sequence 84, Appl	332	119.5	631	3	US-09-949-016-6428	Sequence 6428, Ap
260	127.5	6.7	398	4	US-09-905-064A-84	Sequence 84, Appl	333	119.5	631	3	US-09-949-016-6428	Sequence 6428, Ap
261	127.5	6.7	398	4	US-09-905-381A-84	Sequence 84, Appl	334	119.5	631	3	US-09-949-016-6428	Sequence 6428, Ap
262	127.5	6.7	398	4	US-09-906-618A-84	Sequence 84, Appl	335	119.5	631	3	US-09-949-016-6428	Sequence 6428, Ap
263	127.5	6.7	416	4	US-09-638-649-1	Sequence 1, Appli	336	119.5	631	3	US-08-232-538-14	Sequence 14, Appl
264	127.5	6.7	416	4	US-08-755-235-2	Sequence 2, Appli	337	119.5	631	3	US-08-786-164-14	Sequence 14, Appl
265	127.5	6.7	416	4	US-09-638-648-1	Sequence 1, Appli	338	118.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
266	127.5	6.7	432	4	US-09-778-510-2	Sequence 2, Appli	339	118.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
267	127.5	6.7	455	4	US-09-949-016-6949	Sequence 2, Appli	340	118.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
268	127.5	6.7	455	4	US-09-949-016-6949	Sequence 2, Appli	341	118.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
269	127.5	6.7	455	4	US-09-949-016-6949	Sequence 2, Appli	342	118.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
270	127.5	6.7	184	3	US-08-630-172-2	Sequence 2, Appli	343	118.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
271	127.5	6.7	184	3	US-09-375-419-2	Sequence 2, Appli	344	118.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
272	127.5	6.7	252	4	US-09-270-767-44627	Sequence 44627, A	345	118.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
273	127.5	6.7	418	3	US-08-630-172-18	Sequence 18, Appl	346	118.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
274	127.5	6.7	418	3	US-09-375-419-18	Sequence 18, Appl	347	118.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
275	127.5	6.7	1461	4	US-09-976-594-531	Sequence 531, App	348	118.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
276	126	6.6	1651	3	US-09-540-245A-18	Sequence 18, Appl	349	118.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
277	125	6.6	498	4	US-09-354-151-2	Sequence 2, Appli	350	118.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
278	125	6.6	801	3	US-09-383-630-6	Sequence 6, Appli	351	118.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
279	125	6.6	1018	1	US-08-408-093-6	Sequence 6, Appli	352	118.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
280	125	6.6	1018	1	US-08-408-420A-6	Sequence 6, Appli	353	118.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
281	125	6.6	1018	1	US-08-714-901-6	Sequence 6, Appli	354	118.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
282	125	6.6	1018	3	US-08-040-741-6	Sequence 6, Appli	355	118.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
283	124.5	6.5	365	4	US-09-949-016-10321	Sequence 10321, A	356	118.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
284	124.5	6.5	391	3	US-09-949-016-6907	Sequence 6907, Ap	357	118.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
285	124.5	6.5	972	3	US-08-750-141A-2	Sequence 2, Appli	358	118.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
286	124.5	6.5	972	3	US-09-944-807-10	Sequence 10, Appl	359	118.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
287	124	6.5	473	3	US-09-171-945-131	Sequence 131, App	360	118.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
288	124	6.5	519	3	US-08-996-338-21	Sequence 21, Appl	361	118.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
289	124	6.5	519	4	US-09-556-972-21	Sequence 21, Appl	362	118.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
290	124	6.5	537	1	US-08-604-333-4	Sequence 4, Appli	363	118.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
291	124	6.5	537	3	US-09-110-618-4	Sequence 4, Appli	364	118.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
292	124	6.5	537	3	US-09-173-151A-29	Sequence 29, Appl	365	117.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
293	124	6.5	537	4	US-09-578-178-4	Sequence 4, Appli	366	117.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
294	124	6.5	537	4	US-09-577-806-4	Sequence 4, Appli	367	117.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
295	124	6.5	537	4	US-08-621-502-8	Sequence 8, Appli	368	117.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
296	124	6.5	596	2	US-08-752-307B-13	Sequence 13, Appl	369	117.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
297	124	6.5	596	3	US-09-707-802-13	Sequence 13, Appl	370	117.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
298	124	6.5	596	3	US-09-991-326-13	Sequence 13, Appl	371	117.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
299	124	6.5	731	1	US-08-070-165F-10	Sequence 10, Appl	372	117.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
300	124	6.5	731	2	US-08-885-418-10	Sequence 10, Appl	373	117.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
301	123.5	6.5	589	2	US-09-778-510-4	Sequence 10, Appl	374	117.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
302	123.5	6.5	589	2	US-08-724-394A-1	Sequence 1, Appli	375	117.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
303	123	6.4	729	1	US-08-070-165F-6	Sequence 6, Appli	376	116.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
304	123	6.4	729	2	US-08-885-418-6	Sequence 6, Appli	377	116.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
305	123	6.4	1395	3	US-09-540-245A-15	Sequence 15, Appl	378	116.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
306	122.5	6.4	95	3	US-08-928-383B-18	Sequence 18, Appl	379	116.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
307	122.5	6.4	816	1	US-07-640-029-1	Sequence 1, Appli	380	116.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
308	122.5	6.4	1209	4	US-09-130-158A-2	Sequence 2, Appli	381	116.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
309	122	6.4	821	2	US-08-451-822A-13	Sequence 13, Appl	382	116.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
310	122	6.4	821	3	US-08-323-430-13	Sequence 13, Appl	383	116.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
311	121.5	6.4	605	2	US-08-752-307B-8	Sequence 8, Appli	384	116.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
312	121.5	6.4	605	3	US-09-707-802-8	Sequence 8, Appli	385	116.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
313	121.5	6.4	605	3	US-09-991-326-8	Sequence 8, Appli	386	116.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
314	121.5	6.4	643	1	US-08-471-570-6	Sequence 6, Appli	387	116.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
315	121.5	6.4	769	1	US-08-471-570-8	Sequence 8, Appli	388	116.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
316	121	6.3	374	3	US-09-046-736-4	Sequence 4, Appli	389	116.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
317	120	6.3	607	2	US-08-752-307B-12	Sequence 12, Appl	390	116.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
318	120	6.3	607	3	US-09-707-802-12	Sequence 12, Appl	391	116.5	635	4	US-09-949-016-7591	Sequence 7591, Ap
319	120	6.3	607	3	US-09-991-326-12	Sequence 12, Appl	392	116	635	4	US-09-949-016-7591	Sequence 7591, Ap

393	116	6.1	292	4	US-09-800-729-175	Sequence 175, App	466	112.5	5.9	965	4	US-08-467-602-358	Sequence 358, App
394	116	6.1	1018	1	US-08-452-052-2	Sequence 2, Appli	467	112.5	5.9	965	4	US-08-411-295F-284	Sequence 284, App
395	116	6.1	1745	4	US-09-800-729-89	Sequence 89, Appl	468	112	5.9	423	3	US-09-778-510-22	Sequence 22, Appl
396	115.5	6.1	315	4	US-09-949-016-11121	Sequence 11121, A	469	112	5.9	642	1	US-08-217-299-1	Sequence 1, Appli
397	115.5	6.1	315	4	US-09-949-016-11122	Sequence 11122, A	470	112	5.9	647	3	US-08-470-335-243	Sequence 243, App
398	115	6.0	143	4	US-09-949-016-9006	Sequence 9006, Ap	471	112	5.9	647	4	US-08-467-602-308	Sequence 308, App
399	115	6.0	313	4	US-09-756-983-15	Sequence 15, Appl	472	112	5.9	647	4	US-08-411-295F-234	Sequence 234, App
400	115	6.0	459	3	US-08-470-335-239	Sequence 239, App	473	112	5.9	681	4	US-08-467-602-350	Sequence 350, App
401	115	6.0	459	4	US-08-467-602-299	Sequence 299, App	474	112	5.9	681	4	US-08-411-295F-276	Sequence 276, App
402	115	6.0	459	4	US-08-411-295F-225	Sequence 225, App	475	112	5.9	884	3	US-08-470-335-244	Sequence 244, App
403	115	6.0	493	4	US-08-467-602-341	Sequence 341, App	476	112	5.9	864	4	US-08-467-602-309	Sequence 309, App
404	115	6.0	493	4	US-08-411-295F-267	Sequence 267, App	477	112	5.9	864	4	US-08-411-295F-235	Sequence 235, App
405	114.5	6.0	269	4	US-10-000-489-78	Sequence 78, Appl	478	112	5.9	898	4	US-08-467-602-351	Sequence 351, App
406	114.5	6.0	449	3	US-09-310-463-38	Sequence 38, Appl	479	112	5.9	898	4	US-08-411-295F-277	Sequence 277, App
407	114.5	6.0	626	4	US-09-949-016-6213	Sequence 6213, Ap	480	112	5.9	911	3	US-08-470-335-245	Sequence 245, App
408	114.5	6.0	664	4	US-09-949-016-7850	Sequence 7850, Ap	481	112	5.9	911	4	US-08-467-602-310	Sequence 310, App
409	114	6.0	468	3	US-09-232-097-2	Sequence 2, Appli	482	112	5.9	911	4	US-08-467-602-309	Sequence 236, App
410	114	6.0	468	4	US-09-933-561-2	Sequence 2, Appli	483	112	5.9	945	4	US-08-467-602-352	Sequence 352, App
411	114	6.0	946	5	PCT-US95-08493-13	Sequence 13, Appl	484	112	5.9	945	4	US-08-411-295F-278	Sequence 278, App
412	113.5	5.9	280	4	US-09-270-767-43068	Sequence 43068, A	485	111.5	5.8	306	3	US-08-205-697A-17	Sequence 17, Appl
413	113.5	5.9	307	4	US-09-197-970B-3	Sequence 3, Appli	486	111.5	5.8	306	3	US-08-702-525-17	Sequence 17, Appl
414	113.5	5.9	417	4	US-09-949-016-6729	Sequence 6729, Ap	487	111.5	5.8	306	4	US-09-651-200-17	Sequence 17, Appl
415	113.5	5.9	669	1	US-07-847-743B-8	Sequence 8, Appli	488	111.5	5.8	306	4	US-09-667-135-35	Sequence 35, Appl
416	113.5	5.9	669	1	US-07-847-743B-13	Sequence 13, Appl	489	111.5	5.8	306	4	US-09-837-867A-17	Sequence 17, Appl
417	113.5	5.9	669	1	US-08-456-201-8	Sequence 8, Appli	490	111.5	5.8	306	5	PCT-US95-02576-17	Sequence 17, Appl
418	113.5	5.9	669	1	US-08-456-201-13	Sequence 13, Appl	491	111.5	5.8	307	3	US-08-996-338-25	Sequence 25, Appl
419	113.5	5.9	669	2	US-08-330-161-11	Sequence 11, Appl	492	111.5	5.8	307	4	US-09-556-972-25	Sequence 25, Appl
420	113.5	5.9	669	2	US-08-456-241-8	Sequence 8, Appli	493	111.5	5.8	317	4	US-09-684-708A-23	Sequence 23, Appl
421	113.5	5.9	669	2	US-08-456-241-13	Sequence 13, Appl	494	111.5	5.8	342	4	US-09-684-708A-27	Sequence 27, Appl
422	113.5	5.9	669	2	US-08-440-401-11	Sequence 11, Appl	495	111.5	5.8	345	4	US-09-248-796A-18832	Sequence 18832, A
423	113.5	5.9	669	2	US-08-419-878B-11	Sequence 11, Appl	496	111.5	5.8	403	4	US-09-638-649-5	Sequence 5, Appli
424	113.5	5.9	669	3	US-09-173-480-11	Sequence 11, Appl	497	111.5	5.8	403	4	US-09-638-649-5	Sequence 5, Appli
425	113.5	5.9	669	5	PCT-US92-04295A-8	Sequence 8, Appli	498	111.5	5.8	456	3	US-08-470-335-246	Sequence 246, App
426	113.5	5.9	669	5	PCT-US92-04295A-13	Sequence 13, Appl	499	111.5	5.8	456	4	US-08-467-602-303	Sequence 303, App
427	113	5.9	205	4	US-09-451-291-11	Sequence 11, Appl	500	111.5	5.8	456	4	US-08-411-295F-229	Sequence 229, App
428	113	5.9	208	3	US-08-630-172-15	Sequence 15, Appl	501	111.5	5.8	456	4	US-09-949-016-7564	Sequence 7564, Ap
429	113	5.9	208	3	US-09-375-419-15	Sequence 15, Appl	502	111.5	5.8	490	4	US-08-467-602-345	Sequence 345, App
430	113	5.9	208	3	US-09-460-384-36	Sequence 36, Appl	503	111.5	5.8	490	4	US-08-411-295F-271	Sequence 271, App
431	113	5.9	478	5	PCT-US95-08493-15	Sequence 15, Appl	504	111.5	5.8	551	4	US-08-896-537A-2	Sequence 2, Appli
432	113	5.9	860	5	PCT-US95-08493-19	Sequence 19, Appl	505	111.5	5.8	635	3	US-08-470-335-247	Sequence 247, App
433	113	5.9	868	5	PCT-US95-08493-21	Sequence 21, Appl	506	111.5	5.8	635	4	US-08-467-602-302	Sequence 302, App
434	113	5.9	1363	4	US-09-375-248-19	Sequence 19, Appl	507	111.5	5.8	635	4	US-08-411-295F-228	Sequence 228, App
435	112.5	5.9	479	4	US-08-467-602-307	Sequence 307, App	508	111.5	5.8	644	3	US-08-470-335-250	Sequence 250, App
436	112.5	5.9	479	4	US-08-411-295F-233	Sequence 233, App	509	111.5	5.8	644	4	US-08-467-602-311	Sequence 311, App
437	112.5	5.9	490	4	US-08-667-135-28	Sequence 28, Appl	510	111.5	5.8	644	4	US-08-411-295F-237	Sequence 237, App
438	112.5	5.9	513	4	US-08-467-602-349	Sequence 349, App	511	111.5	5.8	651	4	US-09-270-767-44877	Sequence 44877, A
439	112.5	5.9	513	4	US-08-411-295F-275	Sequence 275, App	512	111.5	5.8	669	4	US-08-467-602-344	Sequence 344, App
440	112.5	5.9	650	3	US-09-310-463-2	Sequence 2, Appli	513	111.5	5.8	669	4	US-08-411-295F-270	Sequence 270, App
441	112.5	5.9	650	4	US-08-842-248A-2	Sequence 2, Appli	514	111.5	5.8	678	4	US-08-467-602-353	Sequence 353, App
442	112.5	5.9	651	3	US-08-985-950-22	Sequence 22, Appl	515	111.5	5.8	678	4	US-08-411-295F-279	Sequence 279, App
443	112.5	5.9	651	4	US-09-546-049-22	Sequence 22, Appl	516	111.5	5.8	782	4	US-09-684-708A-21	Sequence 21, Appl
444	112.5	5.9	658	4	US-08-467-602-305	Sequence 305, App	517	111.5	5.8	823	3	US-08-470-335-248	Sequence 248, App
445	112.5	5.9	658	4	US-08-411-295F-231	Sequence 231, App	518	111.5	5.8	852	4	US-08-467-602-300	Sequence 300, App
446	112.5	5.9	667	4	US-08-467-602-314	Sequence 314, App	519	111.5	5.8	852	4	US-08-411-295F-226	Sequence 226, App
447	112.5	5.9	667	4	US-08-411-295F-240	Sequence 240, App	520	111.5	5.8	861	3	US-08-470-335-251	Sequence 251, App
448	112.5	5.9	692	4	US-08-467-602-347	Sequence 347, App	521	111.5	5.8	861	4	US-08-467-602-312	Sequence 312, App
449	112.5	5.9	692	4	US-08-411-295F-273	Sequence 273, App	522	111.5	5.8	861	4	US-08-411-295F-238	Sequence 238, App
450	112.5	5.9	701	4	US-08-467-602-356	Sequence 356, App	523	111.5	5.8	886	4	US-08-467-602-342	Sequence 342, App
451	112.5	5.9	701	4	US-08-411-295F-282	Sequence 282, App	524	111.5	5.8	886	4	US-08-411-295F-268	Sequence 268, App
452	112.5	5.9	875	4	US-08-467-602-306	Sequence 306, App	525	111.5	5.8	895	4	US-08-467-602-354	Sequence 354, App
453	112.5	5.9	875	4	US-08-467-602-322	Sequence 232, App	526	111.5	5.8	895	4	US-08-411-295F-280	Sequence 280, App
454	112.5	5.9	884	4	US-08-467-602-315	Sequence 315, App	527	111.5	5.8	899	3	US-08-470-335-249	Sequence 249, App
455	112.5	5.9	884	4	US-08-411-295F-241	Sequence 241, App	528	111.5	5.8	899	4	US-08-467-602-301	Sequence 301, App
456	112.5	5.9	909	4	US-08-467-602-348	Sequence 348, App	529	111.5	5.8	899	4	US-08-411-295F-227	Sequence 227, App
457	112.5	5.9	909	4	US-08-411-295F-274	Sequence 274, App	530	111.5	5.8	908	3	US-08-470-335-252	Sequence 252, App
458	112.5	5.9	918	4	US-08-467-602-357	Sequence 357, App	531	111.5	5.8	908	4	US-08-467-602-313	Sequence 313, App
459	112.5	5.9	918	4	US-08-411-295F-283	Sequence 283, App	532	111.5	5.8	908	4	US-08-411-295F-239	Sequence 239, App
460	112.5	5.9	922	4	US-08-467-602-304	Sequence 304, App	533	111.5	5.8	933	4	US-08-467-602-343	Sequence 343, App
461	112.5	5.9	922	4	US-08-411-295F-230	Sequence 230, App	534	111.5	5.8	933	4	US-08-411-295F-269	Sequence 269, App
462	112.5	5.9	931	4	US-08-467-602-316	Sequence 316, App	535	111.5	5.8	942	4	US-08-467-602-355	Sequence 355, App
463	112.5	5.9	931	4	US-08-411-295F-242	Sequence 242, App	536	111.5	5.8	942	4	US-08-411-295F-281	Sequence 281, App
464	112.5	5.9	956	4	US-08-467-602-346	Sequence 346, App	537	111.5	5.8	1241	3	US-09-040-774-2	Sequence 2, Appli
465	112.5	5.9	956	4	US-08-411-295F-272	Sequence 272, App	538	110.5	5.8	306	2	US-08-147-772-4	Sequence 4, Appli



539	110.5	5.8	306	2	US-08-456-104-8	Sequence 8, Appli	612	108.5	5.7	625	2	US-08-456-241-26	Sequence 26, Appli
540	110.5	5.8	306	2	US-08-101-624-25	Sequence 25, Appli	613	108.5	5.7	625	5	PCT-US92-04295A-26	Sequence 26, Appli
541	110.5	5.8	306	3	US-08-153-262-4	Sequence 4, Appli	614	108.5	5.7	640	4	US-08-467-602-256	Sequence 256, App
542	110.5	5.8	306	3	US-08-479-744A-31	Sequence 31, Appli	615	108.5	5.7	640	4	US-08-411-295F-182	Sequence 182, App
543	110.5	5.8	306	3	US-08-280-757B-31	Sequence 31, Appli	616	108.5	5.7	646	4	US-09-949-016-6728	Sequence 6728, Ap
544	110.5	5.8	306	3	US-09-159-135-4	Sequence 4, Appli	617	108.5	5.7	646	4	US-09-653-961-4	Sequence 4, Appli
545	110.5	5.8	306	3	US-09-450-798-4	Sequence 4, Appli	618	108.5	5.7	687	4	US-08-467-602-254	Sequence 254, App
546	110.5	5.8	306	4	US-09-425-762-31	Sequence 31, Appli	619	108.5	5.7	687	4	US-08-411-295F-180	Sequence 180, App
547	110.5	5.8	306	4	US-08-453-386A-4	Sequence 4, Appli	620	108.5	5.7	746	3	US-08-434-000A-4	Sequence 4, Appli
548	110.5	5.8	306	4	US-09-206-132-8	Sequence 8, Appli	621	108.5	5.7	746	3	US-09-312-157-4	Sequence 4, Appli
549	110.5	5.8	306	4	US-09-425-516-31	Sequence 31, Appli	622	108.5	5.7	746	4	US-09-717-888-4	Sequence 4, Appli
550	110.5	5.8	758	3	US-08-874-678-1	Sequence 1, Appli	623	108.5	5.7	764	4	US-09-949-016-6254	Sequence 6254, Ap
551	110.5	5.8	758	3	US-08-643-839-1	Sequence 1, Appli	624	108	5.7	330	2	US-08-332-562A-81	Sequence 81, Appli
552	110.5	5.8	758	3	US-09-351-363-24	Sequence 24, Appli	625	108	5.7	330	2	US-08-332-562A-134	Sequence 134, App
553	110.5	5.8	758	3	US-09-348-886-1	Sequence 1, Appli	626	108	5.7	483	3	US-09-310-463-16	Sequence 16, Appli
554	110.5	5.8	868	2	US-08-374-834-1	Sequence 1, Appli	627	108	5.7	483	3	US-08-842-248A-16	Sequence 16, Appli
555	110.5	5.8	868	2	US-08-644-271-1	Sequence 1, Appli	628	108	5.7	483	4	US-09-949-016-11206	Sequence 11206, A
556	110.5	5.8	868	4	US-09-077-955-1	Sequence 1, Appli	629	108	5.7	621	1	US-09-653-961-2	Sequence 2, Appli
557	110.5	5.8	869	4	US-09-715-249-8	Sequence 8, Appli	630	107.5	5.6	221	1	US-08-168-091A-4	Sequence 4, Appli
558	110.5	5.8	1617	4	US-09-784-358-16	Sequence 16, Appli	631	107.5	5.6	303	4	US-09-651-200-23	Sequence 23, Appli
559	110.5	5.8	1691	4	US-08-484-358-2	Sequence 2, Appli	632	107.5	5.6	303	4	US-09-441-411-15	Sequence 15, Appli
560	110	5.8	212	4	US-09-949-016-10458	Sequence 10458, A	633	107.5	5.6	303	4	US-09-441-411-20	Sequence 20, Appli
561	110	5.8	301	3	US-08-829-525-24	Sequence 24, Appli	634	107.5	5.6	309	2	US-08-456-104-4	Sequence 4, Appli
562	110	5.8	301	3	US-08-609-583A-24	Sequence 24, Appli	635	107.5	5.6	309	3	US-08-479-744A-23	Sequence 23, Appli
563	110	5.8	301	3	US-08-937-399-24	Sequence 24, Appli	636	107.5	5.6	309	3	US-08-280-757B-23	Sequence 23, Appli
564	110	5.8	301	4	US-09-310-367-24	Sequence 24, Appli	637	107.5	5.6	309	3	US-08-205-697A-21	Sequence 21, Appli
565	110	5.8	301	4	US-09-032-337-24	Sequence 24, Appli	638	107.5	5.6	309	3	US-08-702-525-21	Sequence 21, Appli
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567	110	5.8	597	4	US-09-746-311B-381	Sequence 381, App	640	107.5	5.6	309	4	US-09-667-135-33	Sequence 33, Appli
568	110	5.8	924	1	US-08-481-130-28	Sequence 28, Appli	641	107.5	5.6	309	4	US-09-425-762-23	Sequence 23, Appli
569	110	5.8	924	1	US-08-656-984A-28	Sequence 28, Appli	642	107.5	5.6	309	4	US-09-837-867A-21	Sequence 21, Appli
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571	110	5.8	924	3	US-08-487-595-28	Sequence 28, Appli	644	107.5	5.6	309	4	US-09-441-411-13	Sequence 13, Appli
572	109.5	5.7	320	3	US-08-205-697A-2	Sequence 2, Appli	645	107.5	5.6	309	4	US-09-441-411-18	Sequence 18, Appli
573	109.5	5.7	320	3	US-08-702-525-2	Sequence 2, Appli	646	107.5	5.6	309	4	US-09-441-411-24	Sequence 24, Appli
574	109.5	5.7	320	4	US-09-837-867A-2	Sequence 2, Appli	647	107.5	5.6	309	4	US-09-425-516-23	Sequence 13, Appli
575	109.5	5.7	320	5	PCT-US95-02576-2	Sequence 2, Appli	648	107.5	5.6	309	5	PCT-US95-02576-21	Sequence 21, Appli
576	109.5	5.7	332	4	US-09-062-365-1	Sequence 1, Appli	649	107.5	5.6	314	3	US-08-205-697A-13	Sequence 13, Appli
577	109	5.7	440	4	US-09-866-028-61	Sequence 61, Appli	650	107.5	5.6	314	3	US-08-702-525-13	Sequence 13, Appli
578	109	5.7	440	4	US-09-944-457-61	Sequence 61, Appli	651	107.5	5.6	314	4	US-09-837-867A-13	Sequence 13, Appli
579	109	5.7	442	4	US-09-778-510-20	Sequence 20, Appli	652	107.5	5.6	314	4	US-09-441-411-14	Sequence 14, Appli
580	109	5.7	442	4	US-09-930-803-1	Sequence 1, Appli	653	107.5	5.6	314	4	US-09-441-411-19	Sequence 19, Appli
581	109	5.7	652	3	US-09-310-463-4	Sequence 4, Appli	654	107.5	5.6	314	5	PCT-US95-02576-13	Sequence 13, Appli
582	109	5.7	652	4	US-08-842-248A-4	Sequence 4, Appli	655	107.5	5.6	323	4	US-09-684-708A-25	Sequence 25, Appli
583	109	5.7	869	1	US-08-374-834-16	Sequence 16, Appli	656	107.5	5.6	356	4	US-09-441-411-11	Sequence 11, Appli
584	109	5.7	869	2	US-08-644-271-29	Sequence 29, Appli	657	107.5	5.6	356	4	US-09-441-411-12	Sequence 12, Appli
585	109	5.7	869	4	US-09-077-955-33	Sequence 33, Appli	658	107.5	5.6	356	4	US-09-441-411-16	Sequence 16, Appli
586	109	5.7	1298	1	US-08-222-616-33	Sequence 33, Appli	659	107.5	5.6	356	4	US-09-441-411-17	Sequence 17, Appli
587	109	5.7	1298	1	US-08-340-011-2	Sequence 2, Appli	660	107.5	5.6	489	3	US-09-310-463-14	Sequence 14, Appli
588	109	5.7	1298	3	US-08-901-710-2	Sequence 2, Appli	661	107.5	5.6	489	4	US-08-842-248A-14	Sequence 14, Appli
589	109	5.7	1298	3	US-08-446-648-33	Sequence 33, Appli	662	107.5	5.6	489	4	US-09-949-016-6765	Sequence 6765, Ap
590	109	5.7	1298	4	US-09-982-610-33	Sequence 33, Appli	663	107.5	5.6	630	2	US-08-752-307B-14	Sequence 14, Appli
591	109	5.7	1298	4	US-09-169-079-2	Sequence 2, Appli	664	107.5	5.6	630	3	US-09-707-802-14	Sequence 14, Appli
592	109	5.7	1298	5	PCT-US95-04228-33	Sequence 33, Appli	665	107.5	5.6	630	3	US-09-991-326-14	Sequence 14, Appli
593	109	5.7	1362	2	US-08-874-678-33	Sequence 33, Appli	666	107.5	5.6	645	4	US-09-345-473B-15	Sequence 15, Appli
594	109	5.7	1362	3	US-08-643-839-33	Sequence 33, Appli	667	107.5	5.6	645	4	US-09-345-473B-16	Sequence 16, Appli
595	109	5.7	1363	1	US-09-348-886-33	Sequence 33, Appli	668	107.5	5.6	732	1	US-07-847-743B-9	Sequence 9, Appli
596	109	5.7	1363	1	US-08-340-011-4	Sequence 4, Appli	669	107.5	5.6	732	1	US-08-456-201-9	Sequence 9, Appli
597	109	5.7	1363	2	US-08-874-678-32	Sequence 32, Appli	670	107.5	5.6	732	2	US-08-456-241-9	Sequence 9, Appli
598	109	5.7	1363	3	US-08-643-839-32	Sequence 32, Appli	671	107.5	5.6	732	5	PCT-US92-04295A-9	Sequence 9, Appli
599	109	5.7	1363	3	US-08-901-710-4	Sequence 4, Appli	672	107.5	5.6	833	4	US-09-949-016-11496	Sequence 11496, A
600	109	5.7	1363	3	US-09-348-886-32	Sequence 32, Appli	673	107.5	5.6	1180	4	US-09-949-016-6577	Sequence 6577, App
601	109	5.7	1363	4	US-09-375-248-2	Sequence 2, Appli	674	107	5.6	244	4	US-08-467-602-257	Sequence 257, App
602	109	5.7	1363	4	US-09-169-079-4	Sequence 4, Appli	675	107	5.6	244	4	US-08-411-295F-183	Sequence 183, App
603	109	5.7	1368	2	US-08-874-678-34	Sequence 34, Appli	676	107	5.6	471	4	US-09-949-016-9042	Sequence 9042, Ap
604	109	5.7	1368	3	US-08-643-839-34	Sequence 34, Appli	677	107	5.6	471	4	US-09-949-016-9043	Sequence 9043, Ap
605	109	5.7	1368	3	US-09-348-886-34	Sequence 34, Appli	678	107	5.6	471	4	US-09-949-016-9044	Sequence 9044, Ap
606	108.5	5.7	344	2	US-08-602-725-34	Sequence 34, Appli	679	107	5.6	471	4	US-09-949-016-9045	Sequence 9045, Ap
607	108.5	5.7	423	4	US-08-467-602-255	Sequence 255, App	680	107	5.6	471	4	US-09-949-016-9046	Sequence 9046, Ap
608	108.5	5.7	423	4	US-08-411-295F-181	Sequence 181, App	681	107	5.6	471	4	US-09-949-016-9047	Sequence 9047, Ap
609	108.5	5.7	467	3	US-09-046-736-2	Sequence 2, Appli	682	107	5.6	471	4	US-09-949-016-9048	Sequence 9048, Ap
610	108.5	5.7	625	1	US-07-847-743B-26	Sequence 26, Appli	683	107	5.6	471	4	US-09-949-016-9049	Sequence 9049, Ap
611	108.5	5.7	625	1	US-08-456-201-26	Sequence 26, Appli	684	107	5.6	471	4	US-09-949-016-9050	Sequence 9050, Ap

685	107	5.6	471	4	US-09-949-016-9051	Sequence 9051, Ap	758	104.5	5.5	241	4	US-08-411-295F-94	Sequence 94, Appl
686	107	5.6	479	4	US-09-723-368-2	Sequence 2, Appli	759	104.5	5.5	249	3	US-09-345-468-9	Sequence 9, Appli
687	107	5.6	479	4	US-09-949-016-6278	Sequence 6278, Ap	760	104.5	5.5	249	3	US-09-414-453A-9	Sequence 9, Appli
688	107	5.6	486	2	US-08-432-016-6	Sequence 6, Appli	761	104.5	5.5	264	4	US-08-467-602-265	Sequence 265, App
689	107	5.6	486	2	US-08-684-594-6	Sequence 6, Appli	762	104.5	5.5	264	4	US-08-411-295F-191	Sequence 191, App
690	107	5.6	522	4	US-09-949-016-7563	Sequence 7563, Ap	763	104.5	5.5	319	3	US-09-345-468-5	Sequence 5, Appli
691	106.5	5.6	349	4	US-09-924-103-4	Sequence 4, Appli	764	104.5	5.5	319	3	US-09-414-453A-5	Sequence 5, Appli
692	106.5	5.6	354	6	5169835-4	Patent No. 5169835	765	104.5	5.5	339	3	US-09-345-468-3	Sequence 3, Appli
693	106.5	5.6	354	6	5169835-4	Patent No. 5169835	766	104.5	5.5	339	3	US-09-414-453A-3	Sequence 3, Appli
694	106.5	5.6	389	4	US-08-467-602-213	Sequence 213, App	767	104.5	5.5	443	4	US-08-467-602-263	Sequence 263, App
695	106.5	5.6	389	4	US-08-411-295F-139	Sequence 139, App	768	104.5	5.5	443	4	US-08-411-295F-189	Sequence 189, App
696	106.5	5.6	606	4	US-08-467-602-214	Sequence 214, App	769	104.5	5.5	452	4	US-08-467-602-272	Sequence 272, App
697	106.5	5.6	606	4	US-08-411-295F-140	Sequence 140, App	770	104.5	5.5	452	4	US-08-411-295F-198	Sequence 198, App
698	106.5	5.6	653	4	US-08-467-602-212	Sequence 212, App	771	104.5	5.5	466	4	US-09-944-807-12	Sequence 12, Appl
699	106.5	5.6	653	4	US-08-411-295F-138	Sequence 138, App	772	104.5	5.5	466	4	US-09-949-016-6766	Sequence 6766, Ap
700	106.5	5.6	816	4	US-09-949-016-8119	Sequence 8119, Ap	773	104.5	5.5	480	4	US-09-949-016-7272	Sequence 7272, Ap
701	106	5.6	283	4	US-09-904-615-106	Sequence 106, App	774	104.5	5.5	579	3	US-09-173-151A-2	Sequence 2, Appli
702	106	5.6	292	4	US-09-651-200-16	Sequence 16, Appl	775	104.5	5.5	609	4	US-09-949-016-7747	Sequence 7747, Ap
703	106	5.6	292	4	US-09-303-040-2	Sequence 2, Appli	776	104.5	5.5	609	4	US-09-949-016-7748	Sequence 7748, Ap
704	106	5.6	292	4	US-09-303-040-4	Sequence 4, Appli	777	104.5	5.5	609	4	US-09-949-016-7749	Sequence 7749, Ap
705	106	5.6	434	3	US-09-540-245A-19	Sequence 19, Appl	778	104.5	5.5	609	4	US-09-949-016-7750	Sequence 7750, Ap
706	105.5	5.5	457	1	US-08-416-478A-8	Sequence 8, Appli	779	104.5	5.5	609	4	US-09-949-016-7751	Sequence 7751, Ap
707	105.5	5.5	457	2	US-08-474-988B-8	Sequence 8, Appli	780	104.5	5.5	609	4	US-09-949-016-7752	Sequence 7752, Ap
708	105.5	5.5	457	2	US-08-394-442B-8	Sequence 8, Appli	781	104.5	5.5	609	4	US-09-949-016-7753	Sequence 7753, Ap
709	105.5	5.5	806	2	US-08-443-861-5	Sequence 5, Appli	782	104.5	5.5	609	4	US-09-949-016-7754	Sequence 7754, Ap
710	105.5	5.5	806	3	US-08-193-829B-5	Sequence 5, Appli	783	104.5	5.5	612	2	US-08-752-307B-11	Sequence 11, Appl
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713	105.5	5.5	917	1	US-08-656-984A-2	Sequence 2, Appli	786	104.5	5.5	660	4	US-08-467-602-264	Sequence 264, App
714	105.5	5.5	917	1	US-08-485-604-2	Sequence 2, Appli	787	104.5	5.5	660	4	US-08-411-295F-190	Sequence 190, App
715	105.5	5.5	917	2	US-08-487-595-2	Sequence 2, Appli	788	104.5	5.5	669	4	US-08-467-602-273	Sequence 273, App
716	105.5	5.5	999	1	US-08-252-626A-2	Sequence 2, Appli	789	104.5	5.5	669	4	US-08-411-295F-199	Sequence 199, App
717	105.5	5.5	999	4	US-09-949-016-6718	Sequence 6718, Ap	790	104.5	5.5	686	3	US-09-173-151A-4	Sequence 4, Appli
718	105.5	5.5	1367	1	US-07-813-593-4	Sequence 4, Appli	791	104.5	5.5	707	4	US-08-467-602-262	Sequence 262, App
719	105.5	5.5	1367	1	US-07-977-451-6	Sequence 6, Appli	792	104.5	5.5	707	4	US-08-411-295F-188	Sequence 274, App
720	105.5	5.5	1367	1	US-07-946-507-4	Sequence 4, Appli	793	104.5	5.5	716	4	US-08-467-602-274	Sequence 280, App
721	105.5	5.5	1367	1	US-08-252-517-6	Sequence 6, Appli	794	104.5	5.5	716	4	US-08-411-295F-200	Sequence 200, App
722	105.5	5.5	1367	1	US-07-906-397A-6	Sequence 6, Appli	795	104.5	5.5	1268	3	US-08-506-296B-28	Sequence 28, Appl
723	105.5	5.5	1367	1	US-08-601-891-6	Sequence 6, Appli	796	104	5.5	212	3	US-08-702-525-63	Sequence 63, Appl
724	105.5	5.5	1367	2	US-08-443-861-2	Sequence 2, Appli	797	104	5.5	212	5	PCT-US95-02576-63	Sequence 63, Appl
725	105.5	5.5	1367	2	US-09-021-324-6	Sequence 2, Appli	798	104	5.5	226	5	PCT-US95-02576-65	Sequence 65, Appl
726	105.5	5.5	1367	2	US-08-193-829B-6	Sequence 2, Appli	799	104	5.5	226	5	PCT-US95-02576-65	Sequence 65, Appl
727	105.5	5.5	1367	4	US-09-872-136B-6	Sequence 6, Appli	800	104	5.5	227	4	US-09-205-258-947	Sequence 947, App
728	105.5	5.5	1367	5	PCT-US92-02750-8	Sequence 8, Appli	801	104	5.5	240	1	US-08-471-570-12	Sequence 12, Appl
729	105.5	5.5	1367	5	PCT-US92-05401-6	Sequence 6, Appli	802	104	5.5	270	3	US-09-430-503-26	Sequence 26, Appl
730	105.5	5.5	1367	5	PCT-US92-09893-6	Sequence 6, Appli	803	104	5.5	270	3	US-09-430-503-30	Sequence 30, Appl
731	105	5.5	210	4	US-08-467-602-215	Sequence 215, App	804	104	5.5	283	2	US-09-332-562A-136	Sequence 136, App
732	105	5.5	210	4	US-08-411-295F-141	Sequence 141, App	805	104	5.5	355	1	US-08-471-570-14	Sequence 14, Appl
733	105	5.5	277	4	US-09-354-151-3	Sequence 3, Appli	806	104	5.5	432	4	US-08-467-602-266	Sequence 266, App
734	105	5.5	323	4	US-09-651-200-21	Sequence 21, Appl	807	104	5.5	432	4	US-08-411-295F-192	Sequence 192, App
735	105	5.5	323	4	US-09-441-411-22	Sequence 22, Appl	808	104	5.5	489	4	US-09-667-135-30	Sequence 30, Appl
736	105	5.5	323	5	PCT-US94-09642-2	Sequence 2, Appli	809	104	5.5	501	3	US-08-891-845-10	Sequence 10, Appl
737	105	5.5	329	2	US-08-456-104-2	Sequence 2, Appli	810	104	5.5	501	4	US-09-514-573-10	Sequence 10, Appl
738	105	5.5	329	2	US-08-101-624-2	Sequence 2, Appli	811	104	5.5	649	4	US-08-467-602-267	Sequence 267, App
739	105	5.5	329	3	US-08-479-744A-2	Sequence 2, Appli	812	104	5.5	649	4	US-08-411-295F-193	Sequence 193, App
740	105	5.5	329	3	US-08-280-757B-2	Sequence 2, Appli	813	104	5.5	696	4	US-08-467-602-268	Sequence 268, App
741	105	5.5	329	3	US-08-205-697A-23	Sequence 23, Appl	814	104	5.5	696	4	US-08-411-295F-194	Sequence 194, App
742	105	5.5	329	3	US-08-702-525-23	Sequence 23, Appl	815	104	5.5	768	3	US-08-811-845-2	Sequence 2, Appli
743	105	5.5	329	3	US-08-403-253A-4	Sequence 4, Appli	816	104	5.5	768	4	US-09-514-573-2	Sequence 2, Appli
744	105	5.5	329	4	US-08-435-816A-4	Sequence 4, Appli	817	103.5	5.4	192	2	US-08-867-680-2	Sequence 2, Appli
745	105	5.5	329	4	US-09-425-762-2	Sequence 2, Appli	818	103.5	5.4	241	4	US-08-467-602-261	Sequence 261, App
746	105	5.5	329	4	US-09-837-867A-23	Sequence 23, Appl	819	103.5	5.4	241	4	US-08-411-295F-187	Sequence 187, App
747	105	5.5	329	4	US-09-206-132-2	Sequence 2, Appli	820	103.5	5.4	420	4	US-08-467-602-260	Sequence 260, App
748	105	5.5	329	4	US-09-441-411-26	Sequence 26, Appl	821	103.5	5.4	420	4	US-08-467-602-260	Sequence 260, App
749	105	5.5	329	4	US-09-425-516-2	Sequence 2, Appli	822	103.5	5.4	422	3	US-08-411-295F-186	Sequence 186, App
750	105	5.5	329	5	PCT-US95-02576-23	Sequence 23, Appl	823	103.5	5.4	422	3	US-08-753-007A-9	Sequence 9, Appli
751	105	5.5	372	4	US-09-949-016-11132	Sequence 11132, A	824	103.5	5.4	429	4	US-09-398-496-9	Sequence 9, Appli
752	105	5.5	1709	4	US-09-949-016-10503	Sequence 10503, A	825	103.5	5.4	429	4	US-08-467-602-269	Sequence 269, App
753	104.5	5.5	241	3	US-08-341-018-54	Sequence 54, Appl	826	103.5	5.4	637	4	US-08-411-295F-195	Sequence 195, App
754	104.5	5.5	241	3	US-08-470-335-195	Sequence 195, App	827	103.5	5.4	637	4	US-08-467-602-258	Sequence 258, App
755	104.5	5.5	241	3	US-08-470-335-195	Sequence 195, App	828	103.5	5.4	645	3	US-08-411-295F-184	Sequence 184, App
756	104.5	5.5	241	4	US-08-467-602-389	Sequence 389, App	829	103.5	5.4	645	3	US-08-753-007A-10	Sequence 10, Appl
757	104.5	5.5	241	4	US-08-411-295F-47	Sequence 47, Appl	830	103.5	5.4	646	4	US-09-398-496-10	Sequence 10, Appl

831	103.5	5.4	646	4	US-08-411-295F-196	Sequence 196, App	904	102	5.3	281	4	US-09-310-367-10	Sequence 10, Appl
832	103.5	5.4	661	2	US-08-793-868-14	Sequence 14, Appl	905	102	5.3	281	4	US-09-032-337-10	Sequence 10, Appl
833	103.5	5.4	661	3	US-09-303-069-14	Sequence 14, Appl	906	102	5.3	281	4	US-09-464-231-10	Sequence 10, Appl
834	103.5	5.4	661	3	US-09-134-250-14	Sequence 14, Appl	907	102	5.3	286	4	US-09-270-767-44618	Sequence 44618, A
835	103.5	5.4	684	4	US-08-467-602-259	Sequence 259, App	908	102	5.3	321	3	US-09-361-434-17	Sequence 17, Appl
836	103.5	5.4	684	4	US-08-411-295F-185	Sequence 185, App	909	102	5.3	321	3	US-09-361-434-22	Sequence 22, Appl
837	103.5	5.4	693	4	US-08-467-602-271	Sequence 271, App	910	102	5.3	321	3	US-09-635-025-17	Sequence 22, Appl
838	103.5	5.4	693	4	US-08-411-295F-197	Sequence 197, App	911	102	5.3	321	3	US-09-635-025-22	Sequence 22, Appl
839	103.5	5.4	805	3	US-08-985-526-34	Sequence 34, Appl	912	102	5.3	329	4	US-09-667-135-32	Sequence 32, Appl
840	103.5	5.4	1447	3	US-09-041-886-25	Sequence 25, Appl	913	102	5.3	332	4	US-09-870-521-3	Sequence 3, Appl
841	103.5	5.4	1447	5	PCT-US94-05277-2	Sequence 2, Appl	914	102	5.3	388	3	US-09-188-930-275	Sequence 275, App
842	103	5.4	524	4	US-09-270-767-44009	Sequence 44009, A	915	102	5.3	388	3	US-09-312-283C-275	Sequence 275, App
843	103	5.4	558	4	US-09-667-135-31	Sequence 31, Appl	916	102	5.3	398	4	US-08-467-602-224	Sequence 224, App
844	103	5.4	645	1	US-07-847-743B-27	Sequence 27, Appl	917	102	5.3	398	4	US-08-411-295F-150	Sequence 150, App
845	103	5.4	645	1	US-08-456-201-27	Sequence 27, Appl	918	102	5.3	615	4	US-08-467-602-225	Sequence 225, App
846	103	5.4	645	1	US-08-428-926-4	Sequence 4, Appl	919	102	5.3	615	4	US-08-411-295F-151	Sequence 151, App
847	103	5.4	645	1	US-08-428-927-4	Sequence 4, Appl	920	102	5.3	662	4	US-08-467-602-226	Sequence 226, App
848	103	5.4	645	1	US-08-428-298-4	Sequence 4, Appl	921	102	5.3	662	4	US-08-411-295F-152	Sequence 152, App
849	103	5.4	645	1	US-08-339-517-4	Sequence 4, Appl	922	101.5	5.3	207	4	US-08-467-602-219	Sequence 219, App
850	103	5.4	645	2	US-08-456-241-27	Sequence 27, Appl	923	101.5	5.3	207	4	US-08-411-295F-145	Sequence 145, App
851	103	5.4	645	3	US-09-020-880-93	Sequence 93, Appl	924	101.5	5.3	226	4	US-09-311-784A-32	Sequence 32, Appl
852	103	5.4	645	3	US-09-101-544-93	Sequence 93, Appl	925	101.5	5.3	232	4	US-09-949-016-7589	Sequence 7589, Ap
853	103	5.4	645	4	US-09-097-681-3	Sequence 3, Appl	926	101.5	5.3	232	4	US-09-949-016-7590	Sequence 7590, Ap
854	103	5.4	645	5	PCT-US92-04295A-27	Sequence 27, Appl	927	101.5	5.3	386	4	US-08-467-602-218	Sequence 218, App
855	102.5	5.4	230	4	US-08-467-602-223	Sequence 223, App	928	101.5	5.3	386	4	US-08-411-295F-144	Sequence 144, App
856	102.5	5.4	230	4	US-08-467-602-223	Sequence 223, App	929	101.5	5.3	603	4	US-08-467-602-216	Sequence 216, App
857	102.5	5.4	241	1	US-08-411-295F-149	Sequence 149, App	930	101.5	5.3	603	4	US-08-411-295F-142	Sequence 142, App
858	102.5	5.4	241	1	US-07-847-743B-30	Sequence 30, Appl	931	101.5	5.3	650	4	US-08-467-602-217	Sequence 217, App
859	102.5	5.4	241	1	US-08-456-201-30	Sequence 30, Appl	932	101.5	5.3	650	4	US-08-411-295F-143	Sequence 143, App
860	102.5	5.4	241	5	US-08-456-241-30	Sequence 30, Appl	933	101	5.3	1187	1	US-08-320-559-28	Sequence 28, Appl
861	102.5	5.4	309	4	PCT-US92-04295A-30	Sequence 30, Appl	934	101	5.3	1187	3	US-08-545-860D-28	Sequence 28, Appl
862	102.5	5.4	309	4	US-09-667-135-6	Sequence 6, Appl	935	101	5.3	1187	5	PCT-US94-04496-28	Sequence 28, Appl
863	102.5	5.4	309	4	US-09-910-174B-7	Sequence 7, Appl	936	101	5.3	1210	1	US-08-320-559-26	Sequence 26, Appl
864	102.5	5.4	318	2	US-09-620-461-7	Sequence 7, Appl	937	101	5.3	1210	3	US-08-545-860D-26	Sequence 26, Appl
865	102.5	5.4	324	4	US-09-610-174B-6	Sequence 6, Appl	938	101	5.3	1210	5	US-09-538-092-1179	Sequence 1179, Ap
866	102.5	5.4	324	4	US-09-920-461-6	Sequence 6, Appl	939	101	5.3	1210	5	PCT-US94-04496-26	Sequence 26, Appl
867	102.5	5.4	325	4	US-09-651-200-20	Sequence 20, Appl	940	101	5.3	1212	1	US-08-072-574-10	Sequence 10, Appl
868	102.5	5.4	340	2	US-08-633-148-2	Sequence 2, Appl	941	101	5.3	1253	3	US-08-506-296B-14	Sequence 14, Appl
869	102.5	5.4	395	4	US-08-467-602-227	Sequence 227, App	942	100.5	5.3	313	4	US-09-701-623C-3	Sequence 3, Appl
870	102.5	5.4	395	4	US-08-411-295F-153	Sequence 153, App	943	100.5	5.3	351	4	US-09-756-983-18	Sequence 18, Appl
871	102.5	5.4	409	4	US-08-467-602-221	Sequence 221, App	944	100.5	5.3	718	1	US-08-190-802A-44	Sequence 44, Appl
872	102.5	5.4	409	4	US-08-411-295F-147	Sequence 147, App	945	100.5	5.3	718	3	US-08-477-346-44	Sequence 44, Appl
873	102.5	5.4	418	4	US-08-467-602-230	Sequence 230, App	946	100.5	5.3	718	4	US-08-473-089-44	Sequence 44, Appl
874	102.5	5.4	418	4	US-08-411-295F-156	Sequence 156, App	947	100.5	5.3	718	4	US-08-487-072A-44	Sequence 44, Appl
875	102.5	5.4	420	1	US-07-847-743B-29	Sequence 29, Appl	948	100.5	5.3	1391	4	US-10-080-505-11	Sequence 11, Appl
876	102.5	5.4	420	1	US-08-456-201-29	Sequence 29, App	949	100.5	5.3	1391	4	US-10-080-505-15	Sequence 15, Appl
877	102.5	5.4	420	2	US-08-456-241-29	Sequence 29, App	950	100.5	5.3	1474	4	US-09-677-046A-4	Sequence 4, Appl
878	102.5	5.4	420	5	PCT-US92-04295A-29	Sequence 29, Appl	951	100.5	5.3	1503	4	US-09-677-046A-6	Sequence 6, Appl
879	102.5	5.4	612	4	US-08-467-602-228	Sequence 228, App	952	100.5	5.3	1509	4	US-09-677-046A-6	Sequence 6, Appl
880	102.5	5.4	612	4	US-08-411-295F-154	Sequence 154, App	953	100	5.2	337	4	US-09-248-796A-15931	Sequence 15931, A
881	102.5	5.4	626	4	US-08-467-602-222	Sequence 222, App	954	100	5.2	424	6	5169835-6	Patent No. 5169835
882	102.5	5.4	626	4	US-08-411-295F-148	Sequence 148, App	955	100	5.2	424	6	5169835-6	Patent No. 5169835
883	102.5	5.4	635	4	US-08-467-602-231	Sequence 231, App	956	100	5.2	547	1	US-08-314-615-1	Sequence 1, Appl
884	102.5	5.4	635	4	US-08-411-295F-157	Sequence 157, App	957	100	5.2	547	1	US-08-314-362-1	Sequence 1, Appl
885	102.5	5.4	637	1	US-07-847-743B-28	Sequence 28, Appl	958	100	5.2	547	1	US-08-433-010-1	Sequence 1, Appl
886	102.5	5.4	637	1	US-08-456-201-28	Sequence 28, Appl	959	100	5.2	547	1	US-08-482-882-1	Sequence 1, Appl
887	102.5	5.4	637	2	US-08-456-241-28	Sequence 28, Appl	960	100	5.2	547	2	US-08-483-389-1	Sequence 1, Appl
888	102.5	5.4	637	5	PCT-US92-04295A-28	Sequence 28, Appl	961	100	5.2	547	2	US-08-487-113D-1	Sequence 1, Appl
889	102.5	5.4	659	4	US-08-467-602-229	Sequence 229, App	962	100	5.2	547	2	US-08-473-503-1	Sequence 1, Appl
890	102.5	5.4	659	4	US-08-411-295F-155	Sequence 155, App	963	100	5.2	547	2	US-08-483-932-1	Sequence 1, Appl
891	102.5	5.4	673	4	US-08-467-602-220	Sequence 220, App	964	100	5.2	547	2	US-08-720-420A-1	Sequence 1, Appl
892	102.5	5.4	673	4	US-08-411-295F-146	Sequence 146, App	965	100	5.2	547	3	US-08-714-017-1	Sequence 1, Appl
893	102.5	5.4	682	4	US-08-467-602-232	Sequence 232, App	966	100	5.2	547	3	US-08-863-790-1	Sequence 1, Appl
894	102.5	5.4	682	4	US-08-411-295F-158	Sequence 158, App	967	100	5.2	547	3	US-08-475-680-1	Sequence 1, Appl
895	102	5.3	176	4	US-09-270-767-59418	Sequence 59418, A	968	100	5.2	547	3	US-08-296-749-1	Sequence 1, Appl
896	102	5.3	270	3	US-09-430-503-28	Sequence 28, Appl	969	100	5.2	547	4	US-08-314-369-1	Sequence 1, Appl
897	102	5.3	270	3	US-09-430-503-32	Sequence 32, Appl	970	100	5.2	598	3	US-09-310-463-10	Sequence 10, Appl
898	102	5.3	281	1	US-08-487-748A-9	Sequence 9, Appl	971	100	5.2	598	4	US-08-842-248A-10	Sequence 10, Appl
899	102	5.3	281	3	US-08-487-748A-10	Sequence 10, Appl	972	100	5.2	615	3	US-08-985-950-16	Sequence 16, Appl
900	102	5.3	281	3	US-08-480-070C-10	Sequence 10, Appl	973	100	5.2	615	3	US-08-985-950-18	Sequence 18, Appl
901	102	5.3	281	3	US-08-829-525-10	Sequence 10, Appl	974	100	5.2	615	4	US-09-546-049-16	Sequence 16, Appl
902	102	5.3	281	3	US-08-609-583A-10	Sequence 10, Appl	975	100	5.2	615	4	US-09-546-049-18	Sequence 18, Appl
903	102	5.3	281	3	US-08-937-399-10	Sequence 10, Appl	976	100	5.2	622	4	US-09-499-846-2	Sequence 2, Appl

977	100	5.2	643	5	PCT-US93-00031-19	Sequence 19, Appl	1050	96	5.0	769	3	US-09-312-157-10	Sequence 10, Appl
978	100	5.2	644	5	PCT-US93-00031-21	Sequence 21, Appl	1051	96	5.0	769	4	US-09-717-888-10	Sequence 10, Appl
979	100	5.2	647	3	US-09-009-430A-91	Sequence 91, Appl	1052	96	5.0	1180	1	US-08-486-270-8	Sequence 8, Appl
980	100	5.2	647	3	US-08-482-073-5	Sequence 5, Appl	1053	96	5.0	1180	3	US-08-367-264-8	Sequence 8, Appl
981	100	5.2	647	5	PCT-US93-00031-11	Sequence 11, Appl	1054	96	5.0	1180	3	US-08-660-148-2	Sequence 2, Appl
982	100	5.2	647	5	PCT-US93-00031-23	Sequence 23, Appl	1055	96	5.0	1180	4	US-09-153-757-8	Sequence 8, Appl
983	99.5	5.2	256	4	US-09-248-796A-14185	Sequence 14185, A	1056	96	5.0	1180	4	US-09-459-715-8	Sequence 8, Appl
984	99.5	5.2	322	4	US-09-667-135-2	Sequence 2, Appl	1057	95.5	5.0	94	3	US-08-928-383B-21	Sequence 21, Appl
985	99.5	5.2	322	4	US-09-910-174B-29	Sequence 29, Appl	1058	95.5	5.0	108	4	US-09-663-600A-191	Sequence 191, App
986	99.5	5.2	322	4	US-09-620-461-29	Sequence 29, Appl	1059	95.5	5.0	269	3	US-09-430-503-2	Sequence 2, Appl
987	99.5	5.2	347	4	US-09-667-135-4	Sequence 4, Appl	1060	95.5	5.0	269	3	US-09-430-503-4	Sequence 4, Appl
988	99.5	5.2	421	3	US-08-659-984A-1	Sequence 1, Appl	1061	95.5	5.0	269	3	US-09-430-503-6	Sequence 6, Appl
989	99.5	5.2	421	3	US-08-660-531-1	Sequence 1, Appl	1062	95.5	5.0	269	3	US-09-430-503-8	Sequence 8, Appl
990	99.5	5.2	444	2	US-08-659-984A-5	Sequence 5, Appl	1063	95.5	5.0	431	3	US-08-985-950-14	Sequence 14, Appl
991	99.5	5.2	444	3	US-08-660-531-5	Sequence 5, Appl	1064	95.5	5.0	431	3	US-08-985-950-20	Sequence 20, Appl
992	99.5	5.2	891	4	US-08-660-531-5	Sequence 25, Appl	1065	95.5	5.0	431	4	US-09-546-049-14	Sequence 14, Appl
993	99	5.2	408	3	US-09-345-473E-25	Sequence 62, Appl	1066	95.5	5.0	431	4	US-09-546-049-20	Sequence 20, Appl
994	99	5.2	419	6	US-09-724-864-62	Sequence 62, Appl	1067	95.5	5.0	451	1	US-08-287-001A-2	Sequence 2, Appl
995	99	5.2	419	6	5169835-2	Patent No. 5169835	1068	95.5	5.0	451	5	PCT-US95-09941-2	Sequence 2, Appl
996	99	5.2	771	3	US-08-434-000A-8	Sequence 8, Appl	1069	95.5	5.0	583	2	US-08-432-016-2	Sequence 2, Appl
997	99	5.2	771	3	US-09-312-157-8	Sequence 8, Appl	1070	95.5	5.0	583	2	US-08-684-594-2	Sequence 2, Appl
998	99	5.2	771	4	US-09-717-888-8	Sequence 8, Appl	1071	95.5	5.0	640	4	US-09-949-016-8243	Sequence 7565, Ap
999	99	5.2	1180	1	US-08-072-574-8	Sequence 32, Appl	1072	95	5.0	101	3	US-08-928-383B-9	Sequence 9, Appl
1000	98.5	5.2	290	4	US-09-910-174B-32	Sequence 32, Appl	1073	95	5.0	247	4	US-09-949-016-6225	Sequence 6225, Ap
1001	98.5	5.2	290	4	US-09-451-291-3	Sequence 3, Appl	1074	95	5.0	247	5	PCT-US94-10257A-2	Sequence 2, Appl
1002	98.5	5.2	290	4	US-09-645-069-23	Sequence 23, Appl	1075	95	5.0	260	4	US-09-949-016-8243	Sequence 8243, Ap
1003	98.5	5.2	611	2	US-08-752-307B-10	Sequence 10, Appl	1076	95	5.0	318	6	5223394-11	Patent No. 5223394
1004	98.5	5.2	611	3	US-09-707-802-10	Sequence 10, Appl	1077	95	5.0	318	6	5223394-11	Patent No. 5223394
1005	98.5	5.2	611	3	US-09-991-326-10	Sequence 10, Appl	1078	95	5.0	471	4	US-09-173-151A-35	Sequence 35, Appl
1006	98	5.1	329	4	US-09-651-200-18	Sequence 18, Appl	1079	95	5.0	668	3	US-09-270-767-43916	Sequence 43916, A
1007	98	5.1	329	4	US-09-303-040-6	Sequence 6, Appl	1080	95	5.0	828	1	US-08-261-304-2	Sequence 2, Appl
1008	98	5.1	351	5	PCT-US93-05703-2	Sequence 2, Appl	1081	95	5.0	906	4	US-09-417-039-11	Sequence 11, Appl
1009	98	5.1	488	4	US-09-499-846-12	Sequence 12, Appl	1082	95	5.0	1090	4	US-09-866-510-14	Sequence 14, Appl
1010	98	5.1	497	4	US-09-499-846-6	Sequence 6, Appl	1083	95	5.0	1106	1	US-08-180-195-2	Sequence 2, Appl
1011	98	5.1	497	4	US-09-499-846-10	Sequence 10, Appl	1084	95	5.0	1106	1	US-08-168-917-2	Sequence 2, Appl
1012	98	5.1	518	3	US-09-240-915-8	Sequence 8, Appl	1085	95	5.0	1106	1	US-08-477-329-2	Sequence 2, Appl
1013	98	5.1	518	3	US-09-591-435-8	Sequence 8, Appl	1086	95	5.0	1106	2	US-08-475-458-2	Sequence 2, Appl
1014	98	5.1	525	4	US-09-499-846-4	Sequence 4, Appl	1087	95	5.0	1106	2	US-08-460-510-2	Sequence 2, Appl
1015	98	5.1	525	4	US-09-499-846-8	Sequence 8, Appl	1088	95	5.0	1106	2	US-08-460-490-2	Sequence 2, Appl
1016	98	5.1	547	1	US-08-473-981A-6	Sequence 6, Appl	1089	95	5.0	1106	3	US-08-980-400-2	Sequence 2, Appl
1017	98	5.1	547	1	US-08-474-087-6	Sequence 10, Appl	1090	95	5.0	1106	3	US-08-462-728-4	Sequence 2, Appl
1018	98	5.1	1212	1	US-08-486-270-10	Sequence 10, Appl	1091	95	5.0	1106	3	US-09-583-459A-2	Sequence 2, Appl
1019	98	5.1	1212	3	US-08-367-264-10	Sequence 5, Appl	1092	95	5.0	1106	3	US-09-583-210-2	Sequence 2, Appl
1020	98	5.1	1212	3	US-08-660-148-5	Sequence 10, Appl	1093	95	5.0	1106	3	US-09-583-449A-2	Sequence 2, Appl
1021	98	5.1	1212	4	US-09-153-757-10	Sequence 10, Appl	1094	95	5.0	1106	3	US-09-435-059-2	Sequence 2, Appl
1022	98	5.1	1212	4	US-09-459-715-10	Sequence 7, Appl	1095	95	5.0	1106	3	US-08-461-917-4	Sequence 4, Appl
1023	98	5.1	1212	4	US-09-695-481-7	Sequence 7, Appl	1096	95	5.0	1106	4	US-08-464-436-4	Sequence 4, Appl
1024	97.5	5.1	281	4	US-09-949-016-8447	Sequence 8447, Ap	1097	95	5.0	1106	4	US-08-464-436-4	Sequence 4, Appl
1025	97.5	5.1	306	4	US-09-369-247-63	Sequence 63, Appl	1098	95	5.0	1106	4	US-09-866-510-18	Sequence 18, Appl
1026	97.5	5.1	307	2	US-08-332-562A-83	Sequence 83, Appl	1099	95	5.0	1106	4	US-09-866-510-20	Sequence 20, Appl
1027	97.5	5.1	313	4	US-09-949-016-10974	Sequence 10974, A	1100	95	5.0	1106	4	US-09-866-510-22	Sequence 22, Appl
1028	97.5	5.1	315	4	US-09-949-016-7014	Sequence 7014, Ap	1101	95	5.0	1106	5	PCT-US94-00730-2	Sequence 2, Appl
1029	97.5	5.1	369	4	US-09-906-779-5	Sequence 4, Appl	1102	95	5.0	1106	5	PCT-US92-00862-2	Sequence 6658, Ap
1030	97.5	5.1	466	2	US-08-432-016-4	Sequence 4, Appl	1103	94.5	5.0	215	4	US-09-949-016-6658	Sequence 10819, A
1031	97.5	5.1	466	2	US-08-684-594-4	Sequence 4, Appl	1104	94.5	5.0	263	3	US-09-345-468-19	Sequence 19, Appl
1032	97.5	5.1	793	1	US-08-188-228-54	Sequence 54, Appl	1105	94.5	5.0	267	3	US-09-414-453A-19	Sequence 19, Appl
1033	97.5	5.1	793	1	US-08-332-643-48	Sequence 48, Appl	1106	94.5	5.0	282	4	US-09-404-879A-393	Sequence 393, App
1034	97.5	5.1	793	1	US-08-332-638-54	Sequence 54, Appl	1107	94.5	5.0	282	4	US-09-667-857-393	Sequence 393, App
1035	97.5	5.1	976	3	US-08-750-141A-1	Sequence 1, Appl	1108	94.5	5.0	292	3	US-09-345-468-18	Sequence 18, Appl
1036	97	5.1	232	3	US-09-361-434-7	Sequence 7, Appl	1109	94.5	5.0	292	3	US-09-414-453A-18	Sequence 18, Appl
1037	97	5.1	232	3	US-09-635-025-7	Sequence 7, Appl	1110	94.5	5.0	299	4	US-09-651-200-15	Sequence 15, Appl
1038	97	5.1	288	1	US-08-396-650-1	Sequence 1, Appl	1111	94.5	5.0	309	4	US-09-404-879A-392	Sequence 392, App
1039	97	5.1	288	1	US-08-768-626-1	Sequence 1, Appl	1112	94.5	5.0	309	4	US-09-667-857-392	Sequence 392, App
1040	97	5.1	288	4	US-09-645-069-12	Sequence 12, Appl	1113	94.5	5.0	313	3	US-09-345-468-16	Sequence 16, Appl
1041	97	5.1	492	3	US-08-462-794-11	Sequence 11, Appl	1114	94.5	5.0	313	3	US-09-414-453A-16	Sequence 16, Appl
1042	97	5.1	715	4	US-09-949-016-7423	Sequence 7423, Ap	1115	94.5	5.0	329	1	US-08-235-477B-3	Sequence 3, Appl
1043	96.5	5.1	261	4	US-09-270-767-32898	Sequence 32898, A	1116	94.5	5.0	329	5	PCT-US95-04353-3	Sequence 3, Appl
1044	96.5	5.1	261	4	US-09-270-767-48115	Sequence 48115, A	1117	94.5	5.0	329	5	US-09-702-705-334	Sequence 334, App
1045	96.5	5.1	340	3	US-09-188-930-184	Sequence 184, App	1118	94.5	5.0	582	4	US-09-736-457-334	Sequence 334, App
1046	96.5	5.1	340	4	US-09-312-283C-184	Sequence 184, App	1119	94.5	5.0	582	4	US-09-614-124B-334	Sequence 334, App
1047	96.5	5.1	613	4	US-09-949-016-7353	Sequence 7353, Ap	1120	94.5	5.0	582	4	US-09-671-325-334	Sequence 334, App
1048	96.5	5.1	651	4	US-09-949-016-8426	Sequence 8426, Ap	1121	94.5	5.0	582	4	US-09-589-184-334	Sequence 334, App
1049	96	5.0	769	3	US-08-434-000A-10	Sequence 10, Appl	1122	94.5	5.0	582	4		

1123	94.5	5.0	582	4	US-09-658-824-334	Sequence 334, App	1196	92	4.8	310	4	US-09-949-016-8501	Sequence 8501, Ap
1124	94.5	5.0	604	4	US-09-949-016-9548	Sequence 9548, Ap	1197	92	4.8	310	4	US-09-949-016-8896	Sequence 8896, Ap
1125	94.5	5.0	954	4	US-09-949-016-6147	Sequence 6147, Ap	1198	92	4.8	322	3	US-09-383-586-33	Sequence 33, Appl
1126	94.5	5.0	961	4	US-09-949-016-7230	Sequence 7230, Ap	1199	92	4.8	322	4	US-09-823-038A-33	Sequence 33, Appl
1127	94.5	5.0	1260	3	US-08-506-296B-21	Sequence 21, Appl	1200	92	4.8	328	1	US-08-225-477B-5	Sequence 5, Appl
1128	94	4.9	272	4	US-09-270-767-36013	Sequence 36013, A	1201	92	4.8	328	5	PCT-US95-04353-5	Sequence 5, Appl
1129	94	4.9	272	4	US-09-270-767-51230	Sequence 51230, A	1202	92	4.8	365	4	US-09-311-021-84	Sequence 84, Appl
1130	94	4.9	529	4	US-09-949-016-6204	Sequence 6204, Ap	1203	92	4.8	528	4	US-09-010-147B-20	Sequence 20, Appl
1131	94	4.9	898	2	US-08-808-982-5	Sequence 5, Appl	1204	92	4.8	703	4	US-10-116-326-6	Sequence 6, Appl
1132	94	4.9	898	3	US-09-306-902A-5	Sequence 5, Appl	1205	92	4.8	762	4	US-10-116-326-6	Sequence 6, Appl
1133	93.5	4.9	96	3	US-08-478-208-4	Sequence 4, Appl	1206	92	4.8	778	4	US-10-116-326-2	Sequence 2, Appl
1134	93.5	4.9	96	3	US-08-921-195-4	Sequence 4, Appl	1207	92	4.8	778	4	US-10-003-690-2	Sequence 2, Appl
1135	93.5	4.9	256	4	US-09-949-016-7326	Sequence 7326, Ap	1208	92	4.8	904	4	US-09-976-594-615	Sequence 615, App
1136	93.5	4.9	355	2	US-08-458-555-2	Sequence 2, Appl	1209	92	4.8	2409	6	5180808-2	Sequence 615, App
1137	93.5	4.9	2842	1	US-07-741-940-7	Sequence 7, Appl	1210	92	4.8	2409	6	5180808-2	Patent No. 5180808
1138	93.5	4.9	2842	1	US-08-289-548A-7	Sequence 7, Appl	1211	91.5	4.8	59	2	US-08-414-657D-52	Sequence 52, Appl
1139	93.5	4.9	2842	1	US-08-452-654-7	Sequence 7, Appl	1212	91.5	4.8	59	2	US-08-414-657D-53	Sequence 53, Appl
1140	93.5	4.9	2842	4	US-08-449-731-7	Sequence 7, Appl	1213	91.5	4.8	157	1	US-08-494-577-4	Sequence 4, Appl
1141	93.5	4.9	2843	1	US-07-741-940-2	Sequence 2, Appl	1214	91.5	4.8	157	1	US-08-494-577-5	Sequence 5, Appl
1142	93.5	4.9	2843	1	US-08-289-548A-2	Sequence 2, Appl	1215	91.5	4.8	157	2	US-08-795-868-4	Sequence 4, Appl
1143	93.5	4.9	2843	1	US-08-452-654-2	Sequence 2, Appl	1216	91.5	4.8	157	2	US-08-795-868-5	Sequence 5, Appl
1144	93.5	4.9	2843	1	US-08-452-655B-2	Sequence 2, Appl	1217	91.5	4.8	157	3	US-09-303-069-5	Sequence 5, Appl
1145	93.5	4.9	2843	1	US-08-452-655B-7	Sequence 7, Appl	1218	91.5	4.8	157	3	US-09-134-250-5	Sequence 5, Appl
1146	93.5	4.9	2843	2	US-08-370-235A-2	Sequence 2, Appl	1219	91.5	4.8	380	4	US-09-877-730-4	Sequence 4, Appl
1147	93.5	4.9	2843	3	US-08-450-582-2	Sequence 2, Appl	1220	91.5	4.8	439	3	US-08-985-950-12	Sequence 12, Appl
1148	93.5	4.9	2843	3	US-08-450-582-7	Sequence 7, Appl	1221	91.5	4.8	439	3	US-09-310-463-8	Sequence 8, Appl
1149	93.5	4.9	2843	4	US-08-449-731-2	Sequence 2, Appl	1222	91.5	4.8	439	4	US-08-842-248A-8	Sequence 8, Appl
1150	93.5	4.9	2843	4	US-10-092-138A-30	Sequence 30, Appl	1223	91.5	4.8	439	4	US-09-546-049-12	Sequence 12, Appl
1151	93.5	4.9	2843	4	US-09-538-092-1007	Sequence 1007, Ap	1224	91.5	4.8	777	2	US-08-874-678-3	Sequence 3, Appl
1152	93.5	4.9	2973	2	US-08-821-355A-7	Sequence 7, Appl	1225	91.5	4.8	777	3	US-08-643-839-3	Sequence 3, Appl
1153	93.5	4.9	2973	3	US-09-003-687A-7	Sequence 7, Appl	1226	91.5	4.8	777	3	US-09-348-886-3	Sequence 3, Appl
1154	93.5	4.9	2973	3	US-09-136-605-7	Sequence 7, Appl	1227	91.5	4.8	830	4	US-09-562-737-35	Sequence 35, Appl
1155	93	4.9	329	1	US-08-348-792-12	Sequence 12, Appl	1228	91.5	4.8	904	4	US-09-877-730-6	Sequence 6, Appl
1156	93	4.9	329	2	US-08-462-738-12	Sequence 12, Appl	1229	91.5	4.8	985	4	US-09-877-730-10	Sequence 10, Appl
1157	93	4.9	329	3	US-09-199-955-12	Sequence 12, Appl	1230	91.5	4.8	1069	4	US-09-877-730-2	Sequence 2, Appl
1158	93	4.9	329	3	US-08-880-875-12	Sequence 12, Appl	1231	91.5	4.8	1150	4	US-09-877-730-8	Sequence 8, Appl
1159	93	4.9	343	1	US-08-348-792-10	Sequence 10, Appl	1232	91	4.8	361	4	US-09-270-767-45128	Sequence 45128, A
1160	93	4.9	343	2	US-08-462-738-10	Sequence 10, Appl	1233	91	4.8	371	4	US-08-411-295F-308	Sequence 308, App
1161	93	4.9	343	3	US-09-199-955-10	Sequence 10, Appl	1234	91	4.8	405	4	US-08-467-602-384	Sequence 384, App
1162	93	4.9	343	3	US-08-880-875-10	Sequence 10, Appl	1235	91	4.8	405	4	US-08-411-295F-307	Sequence 307, App
1163	93	4.9	462	2	US-08-752-307B-7	Sequence 7, Appl	1236	91	4.8	624	2	US-08-642-406A-22	Sequence 22, Appl
1164	93	4.9	462	3	US-09-707-802-7	Sequence 7, Appl	1237	91	4.8	624	3	US-09-199-534-22	Sequence 22, Appl
1165	93	4.9	462	3	US-09-991-326-7	Sequence 7, Appl	1238	91	4.8	624	4	US-09-199-534-22	Sequence 22, Appl
1166	93	4.9	465	2	US-08-752-307B-5	Sequence 5, Appl	1239	91	4.8	709	4	US-09-541-094-14	Sequence 14, Appl
1167	93	4.9	465	3	US-09-707-802-5	Sequence 5, Appl	1240	91	4.8	1106	4	US-09-866-510-16	Sequence 16, Appl
1168	93	4.9	465	3	US-09-991-326-5	Sequence 5, Appl	1241	90.5	4.7	218	4	US-09-451-291-12	Sequence 12, Appl
1169	93	4.9	477	2	US-08-432-016-3	Sequence 3, Appl	1242	90.5	4.7	262	1	US-08-403-379A-1	Sequence 1, Appl
1170	93	4.9	477	2	US-08-684-594-3	Sequence 3, Appl	1243	90.5	4.7	262	2	US-08-929-414-1	Sequence 1, Appl
1171	93	4.9	624	4	US-09-270-767-42659	Sequence 42659, A	1244	90.5	4.7	263	2	US-08-557-309B-51	Sequence 51, Appl
1172	93	4.9	773	3	US-08-434-000A-2	Sequence 2, Appl	1245	90.5	4.7	263	3	US-08-834-306-51	Sequence 51, Appl
1173	93	4.9	773	3	US-09-312-157-2	Sequence 2, Appl	1246	90.5	4.7	263	3	US-08-993-674A-51	Sequence 51, Appl
1174	93	4.9	773	4	US-09-717-888-2	Sequence 2, Appl	1247	90.5	4.7	263	4	US-09-256-976-51	Sequence 51, Appl
1175	93	4.9	799	1	US-08-188-228-42	Sequence 42, Appl	1248	90.5	4.7	334	4	US-09-197-970B-7	Sequence 7, Appl
1176	93	4.9	799	1	US-08-332-638-42	Sequence 42, Appl	1249	90.5	4.7	335	1	US-08-348-792-2	Sequence 2, Appl
1177	93	4.9	915	4	US-08-538-092-63	Sequence 63, Appl	1250	90.5	4.7	335	2	US-08-462-738-2	Sequence 2, Appl
1178	92.5	4.8	192	4	US-09-545-216A-5	Sequence 5, Appl	1251	90.5	4.7	335	3	US-09-199-955-2	Sequence 2, Appl
1179	92.5	4.8	222	4	US-09-545-216A-2	Sequence 2, Appl	1252	90.5	4.7	335	3	US-09-199-955-2	Sequence 2, Appl
1180	92.5	4.8	326	4	US-09-545-216A-6	Sequence 6, Appl	1253	90.5	4.7	335	4	US-08-880-875-2	Sequence 2, Appl
1181	92.5	4.8	828	4	US-10-092-138A-26	Sequence 26, Appl	1254	90.5	4.7	1565	6	5352450-2	Sequence 3, Appl
1182	92.5	4.8	829	1	US-07-670-611-2	Sequence 2, Appl	1255	90.5	4.7	1565	6	5352450-2	Patent No. 5352450
1183	92.5	4.8	829	1	US-08-220-674-2	Sequence 2, Appl	1256	90	4.7	358	4	US-09-719-243-3	Sequence 3, Appl
1184	92.5	4.8	829	1	US-08-445-186-2	Sequence 2, Appl	1257	90	4.7	394	6	5223418-2	Sequence 6, Appl
1185	92.5	4.8	829	1	US-08-446-549-2	Sequence 2, Appl	1258	90	4.7	394	6	5223418-2	Patent No. 5223418
1186	92.5	4.8	829	2	US-08-446-550-2	Sequence 2, Appl	1259	90	4.7	402	3	US-09-292-097-16	Sequence 16, Appl
1187	92	4.8	175	4	US-09-763-902B-6	Sequence 6, Appl	1260	90	4.7	402	4	US-09-933-561-16	Sequence 16, Appl
1188	92	4.8	199	2	US-08-768-964-12	Sequence 12, Appl	1261	90	4.7	432	4	US-09-949-016-6747	Sequence 6747, Ap
1189	92	4.8	199	3	US-09-005-299-12	Sequence 12, Appl	1262	90	4.7	464	2	US-08-602-725-32	Sequence 32, Appl
1190	92	4.8	199	3	US-09-515-431-12	Sequence 12, Appl	1263	90	4.7	464	4	US-09-949-016-6116	Sequence 6116, Ap
1191	92	4.8	218	3	US-08-068-655-7	Sequence 7, Appl	1264	90	4.7	464	4	US-09-949-016-7525	Sequence 7525, Ap
1192	92	4.8	263	2	US-08-768-964-2	Sequence 2, Appl	1265	90	4.7	556	4	US-09-538-092-712	Sequence 712, App
1193	92	4.8	263	3	US-09-005-299-2	Sequence 2, Appl	1266	90	4.7	890	1	US-08-445-640-2	Sequence 2, Appl
1194	92	4.8	263	3	US-09-515-431-2	Sequence 2, Appl	1267	90	4.7	890	3	US-08-170-558-2	Sequence 2, Appl
1195	92	4.8	288	4	US-09-949-016-6579	Sequence 6579, Ap	1268	90	4.7	890	3	US-08-447-314-2	Sequence 2, Appl

1269	90	4.7	890	3	US-08-445-461-2	Sequence 2, Appli	1342	88	4.6	425	3	US-08-470-335-226	Sequence 226, App
1270	90	4.7	890	4	US-08-223-490-2	Sequence 2, Appli	1343	88	4.6	425	4	US-08-467-602-320	Sequence 320, App
1271	90	4.7	911	1	US-08-286-305A-1	Sequence 1, Appli	1344	88	4.6	425	4	US-08-411-295F-246	Sequence 246, App
1272	90	4.7	911	2	US-08-441-104A-1	Sequence 1, Appli	1345	88	4.6	445	4	US-08-467-602-328	Sequence 328, App
1273	90	4.7	911	3	US-08-440-816A-1	Sequence 1, Appli	1346	88	4.6	445	4	US-08-411-295F-254	Sequence 254, App
1274	90	4.7	911	3	US-08-417-381A-1	Sequence 1, Appli	1347	88	4.6	456	4	US-08-467-602-366	Sequence 366, App
1275	90	4.7	1356	1	US-08-810-116-8	Sequence 8, Appli	1348	88	4.6	456	4	US-08-411-295F-292	Sequence 292, App
1276	90	4.7	1356	2	US-07-930-548A-8	Sequence 8, Appli	1349	88	4.6	459	4	US-08-467-602-362	Sequence 362, App
1277	90	4.7	1356	3	US-09-098-707A-2	Sequence 8, Appli	1350	88	4.6	459	4	US-08-411-295F-288	Sequence 288, App
1278	90	4.7	1356	3	US-09-483-539-2	Sequence 2, Appli	1351	88	4.6	479	4	US-08-467-602-370	Sequence 370, App
1279	90	4.7	1356	4	US-09-949-016-6198	Sequence 2, Appli	1352	88	4.6	479	4	US-08-411-295F-296	Sequence 296, App
1280	90	4.7	1356	4	US-09-949-016-9853	Sequence 6198, Ap	1353	88	4.6	601	3	US-08-470-335-233	Sequence 233, App
1281	90	4.7	1456	4	US-09-538-092-1081	Sequence 9853, Ap	1354	88	4.6	601	3	US-08-467-602-323	Sequence 323, App
1282	90	4.7	2090	4	US-08-538-092-1081	Sequence 1081, Ap	1355	88	4.6	601	4	US-08-411-295F-249	Sequence 249, App
1283	89.5	4.7	2120	4	US-08-949-016-9768	Sequence 9768, Ap	1356	88	4.6	601	4	US-08-470-335-227	Sequence 227, App
1284	89.5	4.7	662	1	US-08-430-503-48	Sequence 48, Appl	1357	88	4.6	604	3	US-08-467-602-318	Sequence 318, App
1285	89.5	4.7	735	5	US-08-261-304-7	Sequence 7, Appli	1358	88	4.6	604	4	US-08-467-602-318	Sequence 318, App
1286	89.5	4.7	735	5	PCT-US93-00031-13	Sequence 13, Appl	1359	88	4.6	604	4	US-09-345-473B-17	Sequence 17, Appl
1287	89.5	4.7	739	3	PCT-US93-00031-15	Sequence 15, Appl	1360	88	4.6	610	3	US-08-411-295F-244	Sequence 244, App
1288	89.5	4.7	739	3	US-08-482-073-6	Sequence 6, Appli	1361	88	4.6	610	4	US-08-470-335-236	Sequence 336, App
1289	89.5	4.7	740	5	PCT-US93-00031-9	Sequence 9, Appli	1362	88	4.6	610	4	US-08-467-602-332	Sequence 332, App
1290	89.5	4.7	757	3	US-08-434-000A-6	Sequence 6, Appli	1363	88	4.6	613	3	US-08-411-295F-255	Sequence 255, App
1291	89.5	4.7	757	3	US-09-312-157-6	Sequence 6, Appli	1364	88	4.6	613	4	US-08-411-295F-16	Sequence 16, Appl
1292	89.5	4.7	757	4	US-09-717-888-6	Sequence 6, Appli	1365	88	4.6	622	2	US-08-356-786-16	Sequence 356, App
1293	89.5	4.7	2753	4	US-08-949-016-7659	Sequence 7659, Ap	1366	88	4.6	624	4	US-08-467-602-326	Sequence 326, App
1294	89.5	4.7	2753	4	US-08-949-016-7660	Sequence 7660, Ap	1367	88	4.6	624	4	US-08-411-295F-252	Sequence 252, App
1295	89.5	4.7	3730	4	US-09-949-016-9908	Sequence 9908, Ap	1368	88	4.6	624	4	US-08-467-602-335	Sequence 335, App
1296	89.5	4.7	3924	4	US-09-538-092-1246	Sequence 1246, Ap	1369	88	4.6	633	4	US-08-411-295F-261	Sequence 261, App
1297	89	4.7	174	2	US-08-768-964-13	Sequence 13, Appl	1370	88	4.6	633	4	US-08-467-602-365	Sequence 365, App
1298	89	4.7	174	3	US-09-005-299-13	Sequence 13, Appl	1371	88	4.6	635	4	US-08-411-295F-291	Sequence 291, App
1299	89	4.7	174	3	US-08-515-431-13	Sequence 13, Appl	1372	88	4.6	638	4	US-08-467-602-360	Sequence 360, App
1300	89	4.7	238	2	US-08-768-964-7	Sequence 7, Appli	1373	88	4.6	638	4	US-08-411-295F-286	Sequence 286, App
1301	89	4.7	238	3	US-09-005-299-7	Sequence 7, Appli	1374	88	4.6	644	4	US-08-467-602-374	Sequence 374, App
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1303	89	4.7	525	4	US-09-107-532A-5095	Sequence 5095, Ap	1376	88	4.6	647	4	US-08-467-602-371	Sequence 371, App
1304	89	4.7	626	4	US-09-248-796A-27023	Sequence 27023, A	1377	88	4.6	647	4	US-08-411-295F-297	Sequence 297, App
1305	89	4.7	671	4	US-09-266-225D-16	Sequence 16, Appl	1378	88	4.6	647	4	US-08-467-602-368	Sequence 368, App
1306	89	4.7	907	4	US-08-949-016-9750	Sequence 9750, Ap	1379	88	4.6	658	4	US-08-411-295F-294	Sequence 294, App
1307	89	4.7	907	4	US-09-949-016-9751	Sequence 9751, Ap	1380	88	4.6	658	4	US-08-467-602-377	Sequence 377, App
1308	89	4.7	1457	4	US-09-436-874-2	Sequence 2, Appli	1381	88	4.6	667	4	US-08-411-295F-303	Sequence 303, App
1309	89	4.7	1457	4	US-09-713-273A-18	Sequence 18, Appl	1382	88	4.6	818	3	US-08-470-335-234	Sequence 234, App
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1321	88.5	4.6	722	4	US-09-536-784-84	Sequence 84, Appl	1394	88	4.6	830	4	US-08-411-295F-256	Sequence 256, App
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1324	88	4.6	197	2	US-08-756-387B-11	Sequence 11, Appl	1397	88	4.6	850	4	US-08-467-602-336	Sequence 336, App
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1419 88 4.6 877 3 US-08-470-335-232 Sequence 232, App
1420 88 4.6 877 4 US-08-467-602-331 Sequence 331, App
1421 88 4.6 877 4 US-08-411-295F-257 Sequence 257, App
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1429 88 4.6 899 4 US-08-411-295F-290 Sequence 290, App
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1437 88 4.6 922 4 US-08-411-295F-293 Sequence 293, App
1438 88 4.6 931 4 US-08-467-602-379 Sequence 379, App
1439 88 4.6 931 4 US-08-411-295F-305 Sequence 305, App
1440 88 4.6 978 4 US-08-897-956A-3 Sequence 3, Appl
1441 87.5 4.6 172 2 US-08-756-387B-13 Sequence 13, Appl
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1456 87.5 4.6 361 4 US-08-467-602-248 Sequence 248, App
1457 87.5 4.6 361 4 US-08-411-295F-174 Sequence 174, App
1458 87.5 4.6 395 4 US-08-467-602-290 Sequence 290, App
1459 87.5 4.6 395 4 US-08-411-295F-216 Sequence 216, App
1460 87.5 4.6 455 4 US-09-270-767-44339 Sequence 44339, A
1461 87.5 4.6 578 4 US-08-467-602-249 Sequence 249, App
1462 87.5 4.6 578 4 US-08-411-295F-175 Sequence 175, App
1463 87.5 4.6 612 4 US-08-467-602-291 Sequence 291, App
1464 87.5 4.6 612 4 US-08-411-295F-217 Sequence 217, App
1465 87.5 4.6 625 4 US-08-467-602-250 Sequence 250, App
1466 87.5 4.6 625 4 US-08-411-295F-176 Sequence 176, App
1467 87.5 4.6 659 4 US-08-467-602-292 Sequence 292, App
1468 87.5 4.6 659 4 US-08-411-295F-218 Sequence 218, App
1469 87.5 4.6 879 1 US-08-554-612C-1 Sequence 1, Appl
1470 87.5 4.6 2172 4 US-09-588-110-5266 Sequence 5266, Ap
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1472 87 4.6 120 4 US-09-336-536-45 Sequence 45, Appl
1473 87 4.6 272 4 US-09-248-796A-16689 Sequence 16689, A
1474 87 4.6 307 4 US-09-917-265A-53 Sequence 53, Appl
1475 87 4.6 388 1 US-08-445-640-6 Sequence 6, Appl
1476 87 4.6 388 3 US-08-170-558-6 Sequence 6, Appl
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1480 87 4.6 408 4 US-09-538-092-474 Sequence 474, App
1481 87 4.6 422 1 US-08-036-555B-170 Sequence 170, App
1482 87 4.6 422 1 US-08-469-569-170 Sequence 170, App
1483 87 4.6 422 1 US-08-428-926-3 Sequence 3, Appl
1484 87 4.6 422 1 US-08-249-322A-170 Sequence 170, App
1485 87 4.6 422 1 US-08-428-927-3 Sequence 3, Appl
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1489 87 4.6 422 2 US-08-734-591A-170 Sequence 170, App
1490 87 4.6 422 2 US-08-469-660-170 Sequence 170, App
1491 87 4.6 422 3 US-08-341-018-72 Sequence 72, Appl
1492 87 4.6 422 3 US-08-470-335-170 Sequence 170, App
1493 87 4.6 422 3 US-08-735-021-170 Sequence 170, App
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1497 87 4.6 422 4 US-08-411-295F-65 Sequence 65, Appl
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RESULT 1
US-09-949-016-10605
; Sequence 10605, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE OF INVENTION: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10605
; LENGTH: 894
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10605

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Best Local Similarity 92.5%; Pred. NO. 6.7e-103;
Matches 222; Conservative 2; Mismatches 16; Indels 0; Gaps 0;

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QY 70 HVYNNLTTEQGRVAFASNFLAGDASLQIEPLKPSDEGRYTKVKNSGRYVMSHVILKVL 129
DB 90 HVYNNLTTEQGRVAFASNFLAGDASLQIEPLKPSDEGRYTKVKNSGRYVMSHVILKVL 149
QY 130 VRPSKPKCELGELTEGSDLTLCQESSSGTGPVYVYQRIREKEGEDRLPPKSIDYNNH 189
DB 150 VRPSKPKCELGELTEGSDLTLCQESSSGTGPVYVYQRIREKEGEDRLPPKSIDYNNH 209
QY 190 GPRVLLQNLMTSYSLGYCTAGNEAGKESCVRVTVQVQSIGMVAGAVTGIVACALLIF 249
DB 210 GPRVLLQNLMTSYSLGYCTAGNEAGKESCVRVTVQVQSIGMVAGAVTGIVACALLIF 269

RESULT 2
US-09-899-634C-4
; Sequence 4, Application US/09899634C
; Patent No. 6794186
; GENERAL INFORMATION:
; APPLICANT: Thomas Buhler; Reto Andreas Gadiant; Reinhard Korn; Rao Movva
; TITLE OF INVENTION: PCAR and its uses
; FILE REFERENCE: 4-31499A
; CURRENT APPLICATION NUMBER: US/09/899,634C
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; CURRENT FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: porcine CAR
US-09-859-634C-4

Query Match 24.7%; Score 471; DB 4; Length 365;
Best Local Similarity 32.6%; Pred. No. 7.6e-37;
Matches 124; Conservative 70; Mismatches 154; Indels 32; Gaps 10

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QY 55 --DNEGQNKVVITYSSRHVVNNLTTEEQKGRVAFASNFL-AGDASLIQIEPLKPSDEGRYTC 111
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QY 112 KVRNSGRYVNSHVILKVLVRSPKPKCELEBLTGSDLTLOCSSSGTEPIVYVQWRIRE 171
DB 121 KVKKAPGVGNKKIQLTVLLKPSGRCYVDGSEEIGNDFKLKCEPKGSLPLLYEQKLL-- 178

QY 172 KEGEDERLPPKSRIDYNHGPRVLLQNLTMSYSLGLYQCTAGNEAGKESCVRV-TVQYVQS 230
DB 179 --SNSQKLPTLWLAEMTSP-VISVKNASTEYSGYVCTVKNRVSDDQCLLLDVVPPSNR 235

QY 231 IGVAGAVGTGVAGALLIFLLVWLLIRRKDKERYEEERPNIEIRDAEAPKARLVKPPSS 290
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QY 291 SSGRSRRSGSSSTRTANSASRQRTLSTD--AAPQGLATQAYSLVGPVGRSGEPKKV 348
DB 295 LGSNHSSILGSMSPNMEGYSKTQYNQVPSDFERAPQSPTLPLA-----KV 340

QY 349 HHANLTKAETTPSMIPSOQR 368
DB 341 AAPNLSRMGAVPMVIPAQSK 360

RESULT 3
US-08-928-383B-2
; Sequence 2, Application US/08928383B
; Patent No. 6210921
; GENERAL INFORMATION:
; APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
; APPLICANT: and Marshall S. Horwitz
; TITLE OF INVENTION: CAR, A No. 6210921el Coxsackievirus and Adenovirus
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,383B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,100
; FILING DATE: 13-SEP-1996

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0405 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1946351
; US-08-979-424-3

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Best Local Similarity 31.6%; Pred. No. 2.9e-36;
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Db 121 KVKAPGVANKIHLVVLVSPGARCYYDGSDEEIGSDFKIKCEPKESGLPQYEWQKL-- 178

Qy 172 KEGEDERLPPKSRIDYHNPGRVLLQNLTMSTSGLYQCTAGNEAGKESCVRV-TVQYVQS 230
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Qy 231 IGMVAGAVTGIVAGALLIFLVLWLLIRKDKERYEEERPNREDAEAPKARL----- 284
Db 236 AGLIAGAIIGTLLALALIGLIIFCCRKKRREKEKEVH-HDIREDVPPPKSRTSTARSY 294

Qy 285 --VKPSSSSGSRSSRSGSSSTRSTANSASRSORTLSTDAAPQGLATQAYSLVGPEVRG 342
Db 295 IGSNHSSLGSMSPNMEGYKTOYNQVPSDFERTPQSPITLP----- 336

Qy 343 SEPKKVHHANLTKAETTPSMIPQSQR 368
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RESULT 5
US-09-272-496-2
; Sequence 2, Application US/09272496
; Patent No. 6245966
; GENERAL INFORMATION:
; APPLICANT: DeGregori, James
; TITLE OF INVENTION: Adenoviral mediated gene transfer into lymphocytes
; FILE REFERENCE: 90-98
; CURRENT APPLICATION NUMBER: US/09/272,496
; CURRENT FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: US 60/092782
; EARLIER FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match      24.4%; Score 465; DB 2; Length 365;
Best Local Similarity 31.6%; Pred. No. 2.9e-36;
Matches 122; Conservative 69; Mismatches 151; Indels 44; Gaps 9;

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Db 121 KVKAPGVANKIHLVVLVSPGARCYYDGSDEEIGSDFKIKCEPKESGLPQYEWQKL-- 178

Qy 172 KEGEDERLPPKSRIDYHNPGRVLLQNLTMSTSGLYQCTAGNEAGKESCVRV-TVQYVQS 230
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Qy 285 --VKPSSSSGSRSSRSGSSSTRSTANSASRSORTLSTDAAPQGLATQAYSLVGPEVRG 342
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US-09-272-496-2

Query Match      24.4%; Score 465; DB 3; Length 365;
Best Local Similarity 31.6%; Pred. No. 2.9e-36;
Matches 122; Conservative 69; Mismatches 151; Indels 44; Gaps 9;

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Db 1 MALLLCFVLLCGVVDFAFARLSITTPPEEMIEKAGETAYLPCKFTLSPEDQGPLDIEWLIS 60

Qy 55 --DNEGQKVITYSSRHVYNNLTTEEOKGRVAFASNFL-AGDASLQIEPLKPSDEGRYTC 111
Db 61 PADNQKVDQVILLYSGDKIYDDYDPLDKGRVHFTSNDLKSGDASINVNTNLQSLDIGTYQC 120

Qy 112 KVKNSGRYVWSHVILKVLVRSPKPCLEBELTSGSDLTLOCESSSGTPEIVYVQWIRE 171
Db 121 KVKAPGVANKIHLVVLVSPGARCYYDGSDEEIGSDFKIKCEPKESGLPQYEWQKL-- 178

Qy 172 KEGEDERLPPKSRIDYHNPGRVLLQNLTMSTSGLYQCTAGNEAGKESCVRV-TVQYVQS 230
Db 179 --SDSQMPTSLAEMTSSVISVKNASSEYSGTCTVRNRVSGDQCLLLRVVPPSNK 235

Qy 231 IGMVAGAVTGIVAGALLIFLVLWLLIRKDKERYEEERPNREDAEAPKARL----- 284
Db 236 AGLIAGAIIGTLLALALIGLIIFCCRKKRREKEKEVH-HDIREDVPPPKSRTSTARSY 294

Qy 285 --VKPSSSSGSRSSRSGSSSTRSTANSASRSORTLSTDAAPQGLATQAYSLVGPEVRG 342
Db 295 IGSNHSSLGSMSPNMEGYKTOYNQVPSDFERTPQSPITLP----- 336

Qy 343 SEPKKVHHANLTKAETTPSMIPQSQR 368
Db 337 --PAKVAAPNLSRMGAIPVMIPAQSK 360

RESULT 6
US-09-949-016-6064
; Sequence 6064, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6064
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6064

Query Match      24.4%; Score 465; DB 4; Length 365;
Best Local Similarity 31.6%; Pred. No. 2.9e-36;
Matches 122; Conservative 69; Mismatches 151; Indels 44; Gaps 9;

Qy 1 MSLLLLLLVSYVG-----TLGTHTE-IKRVAEKEVTLPCHHQLGLPEKDTLDIEWLLT 54
Db 1 MALLLCFVLLCGVVDFAFARLSITTPPEEMIEKAGETAYLPCKFTLSPEDQGPLDIEWLIS 60

Qy 55 --DNEGQKVITYSSRHVYNNLTTEEOKGRVAFASNFL-AGDASLQIEPLKPSDEGRYTC 111
Db 61 PADNQKVDQVILLYSGDKIYDDYDPLDKGRVHFTSNDLKSGDASINVNTNLQSLDIGTYQC 120

Qy 112 KVKNSGRYVWSHVILKVLVRSPKPCLEBELTSGSDLTLOCESSSGTPEIVYVQWIRE 171
Db 121 KVKAPGVANKIHLVVLVSPGARCYYDGSDEEIGSDFKIKCEPKESGLPQYEWQKL-- 178

Qy 172 KEGEDERLPPKSRIDYHNPGRVLLQNLTMSTSGLYQCTAGNEAGKESCVRV-TVQYVQS 230
Db 179 --SDSQMPTSLAEMTSSVISVKNASSEYSGTCTVRNRVSGDQCLLLRVVPPSNK 235

Qy 231 IGMVAGAVTGIVAGALLIFLVLWLLIRKDKERYEEERPNREDAEAPKARL----- 284
Db 236 AGLIAGAIIGTLLALALIGLIIFCCRKKRREKEKEVH-HDIREDVPPPKSRTSTARSY 294

Qy 285 --VKPSSSSGSRSSRSGSSSTRSTANSASRSORTLSTDAAPQGLATQAYSLVGPEVRG 342
Db 295 IGSNHSSLGSMSPNMEGYKTOYNQVPSDFERTPQSPITLP----- 336

Qy 343 SEPKKVHHANLTKAETTPSMIPQSQR 368
Db 337 --PAKVAAPNLSRMGAIPVMIPAQSK 360
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Db 121 KVKAPGVANKIHLVILVFKSGARCYVDGSEIEGDFKICEPKESGLPQYEWQKL-- 178
Qy 172 KEGEDERLPPKSRIDYNHGPRVLLQNLMTSGYLYQCTAGNEAGKESCVRV-TVQVQS 230
Db 179 ---SDSQMPTSLAEMTSSTSVISVKNASSEYSGTYSCTVRNRVSGDQCLRLNVPPSNK 235
Qy 231 IGMVAGVTGIVAGALLIFLLVLLIRKDKERYEERPNREDAEAPKARL----- 284
Db 236 AGLIAGAIIGTLLALALIGLIFCCRRKREKEVEH-HDIREDVPPPKSRSTARSY 294
Qy 285 --VKPSSSSGSRSSRSGSSSTRSTANSASQRTLSLTDAAPOGLATQAYSLVGPEVRG 342
Db 295 IGSNHSSILGMSPSNMEGYSKTOYNQVPSDFERTPOSPTLP----- 336
Qy 343 SEPKKVHHLTKAETTPSMIPQSQR 368
Db 337 --PAKVAAPNLSRMGAIPVMIPAQSK 360

RESULT 7
US-09-949-016-11050
; Sequence 11050, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11050
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11050

Query Match 24.4%; Score 465; DB 4; Length 383;
Best Local Similarity 31.6%; Pred. No. 3.1e-36;
Matches 122; Conservative 69; Mismatches 151; Indels 44; Gaps 9;

Qy 1 MSLLLLLLVSYVG-----TLGTHTE-IKRVAREKVTLPCHHQLGLPEKDTLDIEWLLT 54
Db 19 MALLCFVLLCGVDFARSLSTTPEEMIEKAKGETAYLPCKFTLSPEQDGLDIEWLIS 78
Qy 55 --DNEGNOKVITYSSRHVYNNLTBEQGRVAFASNFL-AGDASLQIEPLKPSDGRYTC 111
Db 79 PADNQKVQVILYSGDKIYDDYFDLKGKVHFTSNDLKSGLDASINVTNLQSLDGTQYC 138
Qy 112 KYRNGRYVWSHVILKVLVRPSKPKCELEGELTEGSDLTLOCESSSGTEPIVYVQRIRE 171
Db 139 KVKAPGVANKIHLVILVFKSGARCYVDGSEIEGDFKICEPKESGLPQYEWQKL-- 196
Qy 172 KEGEDERLPPKSRIDYNHGPRVLLQNLMTSGYLYQCTAGNEAGKESCVRV-TVQVQS 230
Db 197 ---SDSQMPTSLAEMTSSTSVISVKNASSEYSGTYSCTVRNRVSGDQCLRLNVPPSNK 253
Qy 231 IGMVAGVTGIVAGALLIFLLVLLIRKDKERYEERPNREDAEAPKARL----- 284
Db 284 AGLIAGAIIGTLLALALIGLIFCCRRKREKEVEH-HDIREDVPPPKSRSTARSY 312
Qy 285 --VKPSSSSGSRSSRSGSSSTRSTANSASQRTLSLTDAAPOGLATQAYSLVGPEVRG 342
Db 313 IGSNHSSILGMSPSNMEGYSKTOYNQVPSDFERTPOSPTLP----- 354
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Qy 343 SEPKKVHHLTKAETTPSMIPQSQR 368
Db 355 --PAKVAAPNLSRMGAIPVMIPAQSK 378

RESULT 8
US-08-928-383B-23
; Sequence 23, Application US/08928383B
; Patent No. 6210921
; GENERAL INFORMATION:
; APPLICANT: Robert W. Pinberg, Jeffrey M. Bergelson,
; APPLICANT: and Marshall S. Horwitz
; TITLE OF INVENTION: CAR, A No. 6210921el Cxsackievirus and Adenovirus
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/928,383B
; APPLICATION NUMBER: US/08/928,383B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,100
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-928-383B-23

Query Match 24.0%; Score 458.5; DB 3; Length 365;
Best Local Similarity 32.3%; Pred. No. 1.2e-35;
Matches 122; Conservative 68; Mismatches 155; Indels 33; Gaps 10;

Qy 3 LILLLLL--VSYYVGLTGTHTEIKRVAE--EKVTLPCHQHQLGLPEKDTLDIEWLL--TD 55
Db 4 LLCFVLLCGIADFTSGLSITTPQRIERAKAGETAYLPCKFTLSPEQDGLDIEWLISPD 63
Qy 56 NEGNOKVITYSSRHVYNNLTBEQGRVAFASNFL-AGDASLQIEPLKPSDEGRYTCVK 114
Db 64 NQIVDQVILYSGDKIYDNYYPDLKGRVHFTSNDVKSGLDASINVTNLQSLDGTQYCKVK 123
Qy 115 NSGRVWVSHVILKVLVRPSKPKCELEGELTEGSDLTLOCESSSGTEPIVYVQRIREK 174
Db 124 KAPGVANKIHLVILVFKSGARCYVDGSEIEGDFKICEPKESGLPQYEWQKL----- 178
Qy 175 EDERLPPKSRIDYNHGPRVLLQNLMTSGYLYQCTAGNEAGKESCVRV-TVQVYQSIGM 233
Db 179 SDSQTMPTSLAEMTSPTSVISVKNASSEYSGTYSCTVRNRVSGDQCLRLNVPPSNRAGT 238
Qy 234 VAGAVTGIVAGALLIFLLVLLIRKDKERYEERPNREDAEAPKARLVKPPSSSSG 293
Db 239 TAGAVIGTLLALVILGAILFCCHRRKREKEVEH-HDIREDVPPPKSRSTARSYIGS 297
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Db 124 KAPGVANKFLLTLVLKPSGTRCFVDSGEIENDFKLCKEPEKGLPLQFQWKL----- 178  
Qy 175 EDERLPKSRIDYHNPGRVLLONLTMSYGLYQCTAGNEAGKESCVRV-TVQYVQSIGM 233  
Db 179 SDSQTMPTSWLAEMTSPVISVKNASSEYSGTCTVQNRVSGDQMLRLDVLVPPSNRAGT 238  
Qy 234 VAGAVTGIVAGALLIFLAVLLIRKDKERYEEREPNEIREDAEAPKARLVKPSSSSSG 293  
Db 239 IAGAVIGTLLALVLGALFCRRKREEKEVH-HDIREDPVPPKSRSTARSYIGS 297  
Qy 294 SRSRSGSSSTRANSASRSQRTLSTD--AAPQ-PGLATQAYSIVGPEVRGSPFKVHH 350  
Db 298 NHSSILGMSPSNMEGYSKTQYNQVPSDFERAPQSPTLA-----PAKPKY 342  
Qy 351 ANLTAKETTPSMIPQSR 368  
Db 343 AYKTDGITVWVWMPAQSK 360

## RESULT 11

US-09-899-634C-2  
; Sequence 2, Application US/09899634C  
; Patent No. 6794186  
; GENERAL INFORMATION:  
; APPLICANT: Thomas Buhler; Reto Andreas Gadiant; Reinhard Korn; Rao Movva  
; TITLE OF INVENTION: PCAR and its uses  
; FILE REFERENCE: 4-31499A  
; CURRENT APPLICATION NUMBER: US/09/899,634C  
; CURRENT FILING DATE: 2002-12-09  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 261  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: delta porcine CAR  
US-09-899-634C-2

Query Match 19.8%; Score 378.5; DB 4; Length 261;  
Best Local Similarity 34.6%; Pred. No. 3.7e-28;  
Matches 91; Conservative 53; Mismatches 104; Indels 15; Gaps 7;

Qy 1 MSLLLLLL---VSYYVTGLGTHTE---IKRVAEEKVTLPCHQHQLPEKDTLDIEWLLT 54  
Db 1 MALLCFVLLCGVADLTRSLSTITPEQMIKAKGETAYLPCRFTLGPEDQGPLDIEWLLS 60  
Qy 55 --DNEGNOKVITYSSRHYNNLTBEQKRVAFASNFL-AGDASLQIEPLKPSDBGRYTC 111  
Db 61 PADNQVDQVILYSGDKYDDYQDLKGRVHFTSNDLKGDSINVTNLQSLDGTGYQC 120  
Qy 112 KYKNSGRYVWSHVILKLVKPSKPCKELEGELEGTEGSDLTLOCESSSGTEPIVYVQRI 171  
Db 121 KVKKAPGVGNKKIQLTVLLKPSGTCYVDGSEIGNDFKLKCEPKESGLPLLYEQKL-- 178  
Qy 172 KEGEDERLPKSRIDYHNPGRVLLONLTMSYGLYQCTAGNEAGKESCVRV-TVQYVQS 230  
Db 179 --SNSQKLPTLWLAEMTSP-VISVKNASTEXTSGTCTVQNRVSGDQCLLRDLVVPPSNR 235  
Qy 231 IGMVAGAVTGIVAGALLIFLVLW 253  
Db 236 AGTIAGVIGVLLALVLGLLIIF 258

## RESULT 12

US-09-604-107A-8  
; Sequence 8, Application US/09604107A  
; Patent No. 6524572  
; GENERAL INFORMATION:  
; APPLICANT: Rainbow Therapeutic Company  
; APPLICANT: Rainbow Therapeutic Company  
; APPLICANT: Li, Yibing  
; APPLICANT: Li, Yibing

; TITLE OF INVENTION: Targeting Recombinant Virus with a Bispecific Fusion Protein Ligar  
; TITLE OF INVENTION: Coupling with an Antibody to Cells for Gene Therapy  
; FILE REFERENCE: R7C/DNA001  
; CURRENT APPLICATION NUMBER: US/09/604,107A  
; CURRENT FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 466  
; TYPE: PRT  
; ORGANISM: Homo sapiens, mus and staphylococcus aureus  
US-09-604-107A-8

Query Match 17.8%; Score 340.5; DB 4; Length 466;

Best Local Similarity 27.0%; Pred. No. 4.3e-24;  
Matches 99; Conservative 66; Mismatches 158; Indels 43; Gaps 10;

Qy 23 IKRVAEEKVTLPCHQHQLPEKDTLDIEWLLT--DNEGNOKVITYSSRHYNNLTREQK 80  
Db 104 IEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPADNQKVDQVILYSGDKIYDYPDLK 163  
Qy 81 GRVAFASNFL-AGDASLQIEPLKPSDBGRYTCVKNRGYVWSHVILKLVKPSKPCKE 139  
Db 164 GRVHFTSNDLKGDSINVTNLQSLDGTGYQCKVKAPGVANKKIHLVLLVKPSGARCYV 223  
Qy 140 EGELEGSDLTLOCESSSGTEPIVYVQRIKREGEDELERLPKSRIDYHNPGRVLLQNT 199  
Db 224 DGSSEIGSDFKICEPKESGLFQYEQKL-----SDSQKMTSWLAEMTSSVISVKNAS 278  
Qy 200 MSYSGLYQCTAGNEAGKESCVRV-TVQYVQSIGMVAGAVTGIVAGALLIFLVLWLLIRR 258  
Db 279 SEYSGTCTVNRVSGDQCLLRNVPPSNKAGLIAAPKSTPPGSSA-----AADNK 332  
Qy 259 KDKER----YE-----BEERPNEIR--EDAEAPKARLVKPSSSSGSRSSSGSSST 304  
Db 333 FNKEQONAFYEILHLPNLNEEQRNAFIQSLKDDPSQSANLLAEAKLNDQAQAPKVDNKEN 392  
Qy 305 RSTAN-----SASRSOR-----TLSTDAAQPGLATQAYSIVGPEVRGSEPKVHH 350  
Db 393 KEQONAFYEILHLPNLNEEQRNAFIQSLKDDPSQSANLLAEAKLNDQAQAPNLEQKLISE 452  
Qy 351 ANLTAKA 356  
Db 453 EDLNSA 458

## RESULT 13

US-09-336-536-40  
; Sequence 40, Application US/09336536  
; Patent No. 6406884  
; GENERAL INFORMATION:  
; APPLICANT: Leidy, K.  
; APPLICANT: McKay, C.  
; APPLICANT: Bossone, S.  
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF  
; FILE REFERENCE: 7853-144  
; CURRENT APPLICATION NUMBER: US/09/336,536  
; CURRENT FILING DATE: 1999-06-18  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 40  
; LENGTH: 365  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-336-536-40

Query Match 16.8%; Score 321; DB 4; Length 365;

Best Local Similarity 28.4%; Pred. No. 2.2e-22;  
Matches 108; Conservative 57; Mismatches 153; Indels 62; Gaps 12;

Qy 22 EIKRVAEEKVTLPCHQHQLPE-----KDTLDIEWLLTDSNGNQKVITYSSRHYNNLT 76  
Db 12 KLEAVEGEVVLPAWYTMAREBSWHPREVPIILWFLFQEGKEGKPNQVLSYINGVMTN--- 68



Db 233 MNVALYVGIAVGVAALIIIGIIIIYCCCRGKDDNTEDKEDARN--REAYEPEQL 288

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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : Published Applications AA:\*

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3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1908	100.0	373	9	US-09-796-858-24
33	1908	100.0	373	10	US-09-997-428-503
128	1908	100.0	373	14	US-10-167-749-59
290	1908	100.0	373	14	US-10-223-085-64
296	1908	100.0	373	14	US-10-219-065-130
325	1908	100.0	373	14	US-10-223-084-64
326	1908	100.0	373	14	US-10-223-088-64
337	1908	100.0	373	14	US-10-223-090-64
332	1908	100.0	373	14	US-10-223-087-64
334	1908	100.0	373	14	US-10-223-083-64
337	1908	100.0	373	14	US-10-223-089-64
508	1908	100.0	373	14	US-10-223-081-64
546	1908	100.0	373	14	US-10-223-082-64
615	1908	100.0	373	15	US-10-170-481A-59

617	1908	100.0	373	15	US-10-210-028-59	Sequence 59, Appl
676	1908	100.0	373	15	US-10-162-521A-59	Sequence 59, Appl
685	1908	100.0	373	15	US-10-305-654-64	Sequence 64, Appl
700	1908	100.0	373	15	US-10-081-056-64	Sequence 64, Appl
707	1908	100.0	373	16	US-10-696-487-2	Sequence 2, Appl
709	1908	100.0	373	17	US-10-918-851-59	Sequence 59, Appl
710	1908	100.0	373	17	US-10-931-886-388	Sequence 388, Appl
711	1908	100.0	373	17	US-10-805-667-59	Sequence 59, Appl
712	1908	100.0	373	17	US-10-897-359-59	Sequence 59, Appl
714	1908	100.0	373	17	US-10-893-802-59	Sequence 59, Appl
715	1908	100.0	373	17	US-10-897-360-59	Sequence 59, Appl
1763.5	92.4	373	9	US-09-796-858-26	Sequence 26, Appl	
716	692	36.3	141	15	US-10-243-552-499	Sequence 499, Appl
717	670	35.1	139	15	US-10-243-552-930	Sequence 930, Appl
718	471	24.7	365	9	US-09-899-634A-4	Sequence 4, Appl
720	465	24.4	365	9	US-09-971-798-2	Sequence 2, Appl
721	465	24.4	365	14	US-10-176-847-78	Sequence 78, Appl
722	465	24.4	365	17	US-10-482-029-76	Sequence 76, Appl
723	465	24.4	505	14	US-10-114-153-12	Sequence 12, Appl
733	465	24.4	505	14	US-10-114-153-12	Sequence 12, Appl
750	433	22.7	352	10	US-09-997-428-505	Sequence 505, Appl
755	433	22.7	352	13	US-10-053-107-10	Sequence 10, Appl
801	433	22.7	352	14	US-10-213-145-10	Sequence 10, Appl
809	433	22.7	352	14	US-10-213-199-10	Sequence 10, Appl
840	433	22.7	352	14	US-10-223-085-280	Sequence 280, Appl
846	433	22.7	352	14	US-10-219-065-216	Sequence 216, Appl
872	433	22.7	352	14	US-10-223-084-280	Sequence 280, Appl
873	433	22.7	352	14	US-10-223-088-280	Sequence 280, Appl
874	433	22.7	352	14	US-10-223-090-280	Sequence 280, Appl
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885	433	22.7	352	14	US-10-223-081-280	Sequence 280, Appl
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906	433	22.7	352	15	US-10-305-654-280	Sequence 280, Appl
909	433	22.7	352	15	US-10-081-056-280	Sequence 280, Appl
424.5	22.2	422	14	US-10-114-153-14	Sequence 14, Appl	
913	424.5	22.2	422	14	US-10-114-153-14	Sequence 2, Appl
914	378.5	19.8	261	9	US-09-899-634A-2	Sequence 2, Appl
915	362.5	19.0	430	16	US-10-656-269-6	Sequence 2, Appl
916	361	18.9	431	14	US-10-314-395-2	Sequence 2, Appl
917	360	18.9	426	9	US-09-764-853-667	Sequence 667, Appl
918	360	18.9	431	17	US-10-916-064-2	Sequence 2, Appl
919	352.5	18.5	428	16	US-10-656-269-10	Sequence 10, Appl
920	342	17.9	323	9	US-09-971-798-31	Sequence 31, Appl
921	342	17.9	343	9	US-09-971-798-27	Sequence 27, Appl
922	335	17.6	393	14	US-10-270-555-1	Sequence 1, Appl
923	335	17.6	393	14	US-10-270-555-2	Sequence 2, Appl
924	335	17.6	474	14	US-10-270-555-3	Sequence 3, Appl
925	321	16.8	394	10	US-09-796-753-78	Sequence 78, Appl
926	315.5	16.5	326	15	US-10-443-108-4	Sequence 4, Appl
974	309.5	16.2	327	14	US-10-219-065-236	Sequence 236, Appl
1026	309.5	16.2	327	15	US-10-264-237-2730	Sequence 2730, Appl
1031	309.5	16.2	365	9	US-09-925-299-847	Sequence 847, Appl
1032	309.5	16.2	365	10	US-09-925-299-847	Sequence 847, Appl
1033	309.5	16.2	365	14	US-10-106-698-6387	Sequence 6387, Appl
1034	308.5	16.2	319	9	US-09-981-353-65	Sequence 65, Appl
1035	308.5	16.2	319	9	US-09-953-499-6	Sequence 6, Appl
1036	308.5	16.2	319	14	US-10-265-542-6	Sequence 6, Appl
1037	308.5	16.2	319	14	US-10-295-027-1165	Sequence 6, Appl
1038	308.5	16.2	319	16	US-10-633-008-6	Sequence 6, Appl
1039	308.5	16.2	319	16	US-10-785-220-6	Sequence 6, Appl
1040	308.5	16.2	319	16	US-10-785-221-6	Sequence 6, Appl
1041	308.5	16.2	319	16	US-10-785-433-6	Sequence 6, Appl
1042	308.5	16.2	336	15	US-10-363-616-318	Sequence 318, Appl
1043	307.5	16.1	389	10	US-09-892-877-315	Sequence 315, Appl
1044	307.5	16.1	389	10	US-09-948-783-328	Sequence 328, Appl
1047	307.5	16.1	390	9	US-09-905-231A-39	Sequence 39, Appl
1131	307.5	16.1	390	14	US-10-066-269-110	Sequence 110, Appl
1406	307.5	16.1	390	14	US-10-239-976-39	Sequence 39, Appl
1422	307.5	16.1	390	14	US-10-299-937-39	Sequence 39, Appl

Search completed: May 5, 2005, 08:05:08  
Job time : 80 secs

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OM protein - protein search, using sw model

Run on: May 5, 2005, 08:00:39 ; Search time 41 Seconds  
(without alignments)  
875.338 Million cell updates/sec

Title: US-09-978-375A-59

Perfect score: 1908

Sequence: 1 MSLLLLLLVSYVGTLCGH.....TKAETTPMIPSQSRAFOV 373

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	474	24.8	365	2	JC7780
2	196	10.3	299	2	S56749
3	188.5	9.9	338	2	JC5519
4	187	9.8	338	2	JC4776
5	182	9.5	351	1	RWHUC2
6	178	9.3	5175	2	T20992
7	178	9.3	5198	2	T43290
8	163.5	8.6	1323	2	PN0568
9	160	8.4	345	2	S03199
10	159.5	8.4	347	2	S41638
11	159	8.3	713	2	I50128
12	159	8.3	4162	2	T42633
13	158	8.3	345	2	JC4025
14	158	8.3	7962	2	I38346
15	156.5	8.2	526	2	A37821
16	156	8.2	344	2	I56551
17	155	8.1	1896	2	T08851
18	154	8.1	818	2	JC4058
19	153	8.0	1344	2	T14316
20	152.5	8.0	526	2	S70587
21	151.5	7.9	483	2	T17346
22	151	7.9	847	2	JH0371
23	151	7.9	1906	1	S68235
24	149.5	7.8	799	2	S18209
25	148.5	7.8	344	1	RWRTC2
26	148.5	7.8	738	2	A40096
27	148.5	7.8	3707	2	S18252
28	148	7.8	647	2	A35648
29	147	7.7	765	2	C42632
30	147	7.7	812	2	B42632
31	147	7.7	932	2	A42632
32	146.5	7.7	404	1	I61596
33	145	7.6	508	2	A33378
34	143	7.5	338	2	JC1238
35	143	7.5	345	2	JC1239
36	143	7.5	829	2	JC4583
37	142	7.4	868	2	A46512
38	141	7.4	822	2	S19947
39	141	7.4	822	2	B49151
40	140	7.3	1051	2	A39712
41	139.5	7.3	797	2	S38579
42	139.5	7.3	1197	2	T30581
43	138.5	7.3	853	1	IJBONC
44	138	7.2	344	2	B28967
45	138	7.2	1091	1	IJCHNL
46	137	7.2	802	1	TVHUF4
47	137	7.2	1612	2	T30805
48	136.5	7.2	858	1	IJRTNC
49	136	7.1	344	2	I49585
50	135.5	7.1	1070	2	JC4593
51	135.5	7.1	1273	2	T42405
52	135	7.1	518	2	JC4024
53	134.5	7.0	1091	2	A58532
54	134.5	7.0	1330	2	S49010
55	133.5	7.0	1033	2	S19247
56	133	7.0	650	1	JC1450
57	133	7.0	1036	2	S22383
58	133	7.0	1091	2	S01998
59	133	7.0	1333	2	I78875
60	132.5	6.9	980	1	TVCTMD
61	132	6.9	862	2	I49583
62	132	6.9	1651	2	T14160
63	131	6.9	725	2	JE0100
64	131	6.9	1092	1	JN0635
65	131	6.9	4391	2	A38036
66	130.5	6.8	480	2	A56182
67	130.5	6.8	629	2	A46500
68	130.5	6.8	941	1	TVMVMD
69	130	6.8	761	1	IJHUNG
70	129.5	6.8	423	2	T29549
71	129.5	6.8	1499	2	I50212
72	129	6.8	584	2	T08678
73	129	6.8	1338	2	S09982
74	128.5	6.7	480	2	B56182
75	128.5	6.7	521	2	S34338
76	128.5	6.7	813	1	A49123
77	128.5	6.7	1239	1	A32579
78	128	6.7	1501	2	I58148
79	128	6.7	1863	2	S46217
80	128	6.7	1907	2	S50893
81	127.5	6.7	288	2	A45803
82	127.5	6.7	416	1	A42879
83	127.5	6.7	772	2	T13078
84	127	6.7	519	2	A44783
85	127	6.7	806	2	A35963
86	127	6.7	1336	2	I60598
87	126	6.6	725	2	JE0099
88	126	6.6	750	2	S41051
89	126	6.6	800	1	TVHU2F
90	126	6.6	1018	2	JC4211
91	126	6.6	1088	1	IJXNML
92	125.5	6.6	975	1	TVMSKT
93	125	6.6	800	2	A48991
94	125	6.6	801	2	I55363
95	125	6.6	1018	2	A54744
96	124.5	6.5	310	2	JL0119
97	124.5	6.5	725	1	IJWSNG
98	124.5	6.5	816	2	A49151
99	124.5	6.5	972	1	TVHUMD
100	124.5	6.5	1020	2	S05944
101	124.5	6.5	1028	2	I58164
102	124.5	6.5	1115	1	IJWSNL

cell adhesion mole  
cell adhesion mole  
advanced glycosyla  
fasciclin III prec  
opioid-binding pro  
opioid-binding pro  
fibroblast growth  
CD22 homolog/B lym  
fibroblast growth  
fibroblast growth  
kinase-like protei  
neural cell adhesi  
neural cell adhesi  
T-cell surface gly  
neural cell adhesi  
fibroblast growth  
dutt1 protein - mo  
neural cell adhesi  
CD2 antigen protei  
protein-tyrosine k  
sax-3 protein - Ca  
poliovirus recepto  
glial cell membran  
embryonic receptor  
cell adhesion prot  
fibroblast growth  
axonin 1 precursor  
contactin precursor  
receptor tyrosine  
macrophage colony-  
differentiation an  
transmembrane rece  
neural cell adhesi  
neural cell adhesi  
perlecan precursor  
fibroblast growth  
Ly-9.2 antigen - m  
protein-tyrosine k  
neural cell adhesi  
hypothetical prote  
protein-tyrosine-p  
hypothetical prote  
protein-tyrosine k  
fibroblast growth  
biliary glycoprote  
fibroblast growth  
neuroglian - fruct  
protein-tyrosine-p  
protein-tyrosine-p  
protein-tyrosine-p  
B-cell-restricted  
advanced glycosyla  
KIAA0992 protein -  
ecto-ATPase precu  
protein-tyrosine k  
Fit-1 tyrosine kin  
neural cell adhesi  
fibroblast growth  
fibroblast growth  
neural adhesion pr  
neural cell adhesi  
protein-tyrosine k  
heparin-binding gr  
fibroblast growth  
contactin 1 precu  
Fc gamma (IgG) rec  
neural cell adhesi  
fibroblast growth  
macrophage colony-  
neuronal cell surf  
BIG-1 protein - ra  
neural cell adhesi

103	123.5	6.5	821	1	TVMSBK	fibroblast growth	176	112	5.9	286	2	A28333	carcinoembryonic a
104	123	6.4	748	2	S41050	fibroblast growth	177	112	5.9	289	2	G00031	B7 protein - red-c
105	122.5	6.4	1694	2	S50085	sialoadhesin - mou	178	112	5.9	398	2	I49443	gene 2B4 protein -
106	122	6.4	821	1	TVHUF2	fibroblast growth	179	112	5.9	2029	2	TDFELK	B-lymphocyte-p
107	121.5	6.4	240	2	JL0143	antigen BCM1 precu	180	111.5	5.8	309	2	I49503	protein-tyrosine-p
108	121.5	6.4	769	2	S16236	fibroblast growth	181	111.5	5.8	446	2	I45525	B-lymphocyte activ
109	121.5	6.4	822	2	A45081	fibroblast growth	182	111.5	5.8	1241	2	T37190	WSC4 homolog [lmpo
110	121.5	6.4	822	2	A41794	keratinocyte growth	183	111.5	5.8	1880	2	T18531	nephlin - human
111	121.5	6.4	1021	2	A57112	contactin precursor	184	111	5.8	248	1	MPRT0	tractin - medicina
112	121	6.3	841	1	JCS894	killer cell inhibi	185	111	5.8	811	2	A41054	myelin P0 protein
113	120.5	6.3	707	2	A38429	keratinocyte growt	186	111	5.8	873	2	B41054	fasciclin II, tran
114	120.5	6.3	707	2	A54846	fibroblast growth	187	111	5.8	1437	2	T31093	fasciclin II PI-li
115	120.5	6.3	822	2	B54846	fibroblast growth	188	110.5	5.8	729	2	A49120	probable protein-t
116	120.5	6.3	1209	2	T42718	probable neural ce	189	110.5	5.8	871	1	I48696	fibroblast growth
117	120	6.3	330	2	I46691	CD86 precursor - r	190	110.5	5.8	881	1	I48697	protein-tyrosine k
118	120	6.3	521	2	JC1508	biliary glycoprote	191	110.5	5.8	1898	2	S46216	leukocyte antigen-
119	120	6.3	702	2	A36319	carcinoembryonic a	192	110	5.8	238	2	T22098	hypothetical prote
120	120	6.3	806	1	TVHUF3	fibroblast growth	193	110	5.8	270	2	S65739	basigin precursor
121	120	6.3	1040	2	A49356	transient axonal g	194	110	5.8	296	2	I46021	Fc-gamma (IgG) rec
122	120	6.3	1040	2	A34695	axonal glycoprotei	195	110	5.8	330	2	A40071	protein C24A11.8 [
123	119.5	6.3	733	2	I49293	fibroblast growth	196	110	5.8	521	2	F87775	receptor tyrosine
124	119.5	6.3	819	1	TVCHF9	fibroblast growth	197	110	5.8	1040	2	A57638	hypothetical prote
125	119.5	6.3	822	2	I49289	fibroblast growth	198	110	5.8	1103	2	T22889	hypothetical prote
126	119.5	6.3	822	2	S29840	fibroblast growth	199	110	5.8	1173	2	T25893	hypothetical prote
127	119.5	6.3	6642	2	T29757	protein UNC-89 - C	200	110	5.8	2783	2	T34416	hypothetical prote
128	119	6.2	321	2	I54766	B-lymphocyte activ	201	109	5.7	407	2	T08732	myelin-associated
129	119	6.2	823	2	B35963	protein-tyrosine k	202	109	5.7	582	1	BNRT3S	myelin-associated
130	119	6.2	1028	2	A53449	plasmacytoma-assoc	203	109	5.7	626	1	BNRT3	CD0 protein - huma
131	118.5	6.2	344	2	A27681	nonspecific cross-	204	109	5.7	1240	2	T03097	protein-tyrosine k
132	118.5	6.2	487	2	S65133	butyrophilin - mou	205	109	5.7	1298	2	A48999	Fc gamma (IgG) rec
133	118.5	6.2	662	2	C40862	heparin-binding gr	206	108.5	5.7	285	2	S36903	neu differentiatio
134	118.5	6.2	764	2	A49448	irregular chiasm C	207	108.5	5.7	462	2	I38404	cell surface glyco
135	118.5	6.2	789	2	T28714	hypothetical prote	208	108.5	5.7	646	2	I38049	secretory compon
136	118.5	6.2	822	1	TVHUF9	fibroblast growth	209	108.5	5.7	764	1	QRHUGS	sdh protein - frui
137	118.5	6.2	1328	2	T23007	hypothetical prote	210	108.5	5.7	2222	1	T13924	myelin P0 protein
138	118.5	6.2	1355	2	T28715	hypothetical prote	211	108	5.7	330	2	I49660	Fc-gamma-1/gamma-2
139	118	6.2	705	2	S16135	fibroblast growth	212	108	5.7	495	2	A55181	pregnancy-specific
140	117.5	6.2	269	2	A46506	leukocyte activati	213	108	5.7	588	2	JH0506	adhesion molecule
141	117.5	6.2	682	2	A35969	heparin-binding gr	214	108	5.7	588	2	A45254	surface glycoprote
142	117.5	6.2	822	1	TVMSFG	fibroblast growth	215	108	5.7	588	2	A45254	myelin-associated
143	117.5	6.2	832	2	JH0393	fibroblast growth	216	108	5.7	637	2	B33785	fibroblast growth
144	117.5	6.2	6658	2	T13931	projectin - frui	217	108	5.7	812	1	A36477	hypothetical prote
145	117	6.1	244	2	A40428	nonspecific cross-	218	108	5.7	1459	2	T24088	protein unc-52 [im
146	117	6.1	467	1	HLMSF3	poliovirus recepto	219	108	5.7	2295	2	C88369	gene B7-2 protein
147	117	6.1	620	2	JH0593	Schwann cell myeli	220	107.5	5.6	309	2	I49522	biliary glycoprote
148	117	6.1	898	2	A40114	fasciclin II precu	221	107.5	5.6	458	1	WNMSR1	heregulin precurs
149	116.5	6.1	304	1	RWCHH7	cell surface glyco	222	107.5	5.6	640	2	A43271	probable receptor
150	116.5	6.1	417	2	A44194	poliovirus recepto	223	107.5	5.6	645	2	E96631	fibroblast growth
151	116.5	6.1	729	2	A56795	fibroblast growth	224	107.5	5.6	814	1	A39752	neurofascin - chic
152	115.5	6.1	323	2	S06946	Fc gamma (IgG) rec	225	107.5	5.6	1272	2	JC7604	CD86 spliced varia
153	115.5	6.1	392	2	B44194	poliovirus recepto	226	107	5.6	275	2	JC7604	pregnancy-specific
154	115.5	6.1	478	2	I53960	PRR2 alpha - human	227	107	5.6	335	2	H43354	heparin-binding fi
155	115	6.0	1262	1	B48758	protein-tyrosine-p	228	107	5.6	353	2	S51242	heparin-binding fi
156	115	6.0	1496	1	A48758	protein-tyrosine-p	229	107	5.6	599	2	T16774	hypothetical prote
157	114.5	6.0	247	1	A54662	myelin P0 protein	230	107	5.6	1011	2	T13669	hypothetical prote
158	114.5	6.0	530	2	A53437	poliovirus recepto	231	107	5.6	1897	1	TDHULK	leukocyte antigen-
159	114.5	6.0	1379	2	JC4954	vascular endotheli	232	107	5.6	26926	1	I38344	titin, cardiac mus
160	114	6.0	402	2	T09062	probable advanced	233	106.5	5.6	251	2	I38053	myelin protein zer
161	114	6.0	458	2	JC1509	biliary glycoprote	234	106.5	5.6	349	2	I34815	carcinoembryonic a
162	114	6.0	458	2	S68177	C-CAM2a protein is	235	106.5	5.6	351	2	B34595	pregnancy-specific
163	114	6.0	458	2	S23969	cell-adhesion mole	236	106.5	5.6	416	2	G83656	hypothetical prote
164	114	6.0	538	2	JC2457	vascular cell adhe	237	106.5	5.6	824	2	S36439	fibroblast growth
165	114	6.0	626	1	A61084	myelin-associated	238	106.5	5.6	977	2	I45877	protein-tyrosine k
166	114	6.0	820	2	S17295	fibroblast growth	239	106.5	5.6	978	1	A49814	protein-tyrosine k
167	114	6.0	946	1	A47299	ror-related recept	240	105.5	5.5	457	2	A47449	T-cell surface gly
168	114	6.0	3375	1	T19821	hypothetical prote	241	105.5	5.5	999	2	I38547	novel cellular pro
169	113.5	5.9	417	1	RWHUPA	poliovirus recepto	242	105.5	5.5	1015	2	T32186	hypothetical prote
170	113.5	5.9	2051	2	T30938	receptor tyrosine	243	105.5	5.5	1367	2	A41228	protein-tyrosine k
171	113	5.9	364	2	A30521	myeloid cell surfa	244	105.5	5.5	1894	2	C54689	protein-tyrosine-p
172	113	5.9	526	1	A32164	biliary glycoprote	245	105	5.5	219	1	A29128	myelin P0 protein
173	113	5.9	1363	2	I58375	protein-tyrosine k	246	105	5.5	329	1	A48754	B7-2 antigen - hum
174	112.5	5.9	392	1	RWHUPD	poliovirus recepto	247	105	5.5	406	2	E43354	pregnancy-specific
175	112.5	5.9	824	2	S24108	protein-tyrosine k	248	105	5.5	544	2	JC5018	intercellular adhe

249	105	5.5	562	2	T49904	hypothetical prote	322	100	5.2	790	2	A39627	protein-tyrosine k
250	104.5	5.5	241	2	S32359	glial growth facto	323	100	5.2	978	2	S16385	macrophage colony-
251	104.5	5.5	339	2	JC7559	glycoprotein VI-1	324	100	5.2	994	2	I49276	c-mer tyrosine kin
252	104.5	5.5	1268	1	A39640	neural cell adhesi	325	100	5.2	1052	2	B49120	protein-tyrosine k
253	104.5	5.5	1443	2	I50600	neogenin - chicken	326	99.5	5.2	210	2	JG4122	pregnancy-specific
254	104	5.5	283	1	FCWSGI	PC gamma (IgG) rec	327	99.5	5.2	424	2	B36109	pregnancy-specific
255	104	5.5	341	2	JC1511	biliary glycoprote	328	99.5	5.2	540	1	ORHUCR	natriuretic peptid
256	104	5.5	341	2	JC1512	biliary glycoprote	329	99.5	5.2	1021	2	T42634	connectin/titin -
257	104	5.5	426	2	B55181	pregnancy-specific	330	99	5.2	193	2	F89967	hypothetical prote
258	104	5.5	426	2	B55181	pregnancy-specific	331	99	5.2	419	2	A33258	pregnancy-specific
259	104	5.5	426	2	B55181	pregnancy-specific	332	99	5.2	419	2	A33258	pregnancy-specific
260	104	5.5	426	2	B55181	pregnancy-specific	333	99	5.2	426	2	B32258	pregnancy-specific
261	104	5.5	523	2	I50478	neuroilin - goldfis	334	99	5.2	426	2	A35341	pregnancy-specific
262	104	5.5	538	2	I68093	PRR2 delta - human	335	99	5.2	584	2	I50419	s-gigerin precurs
263	104	5.5	1003	2	JH0823	FL-160-2 protein -	336	99	5.2	627	1	A43300	squalene-hopene cy
264	104	5.5	1277	2	T30532	neural cell adhesi	337	99	5.2	635	2	JC5896	killer cell inhibi
265	104	5.5	1912	2	A56178	protein-tyrosine-p	338	99	5.2	917	2	I48950	telencephalin prec
266	104	5.5	3488	2	T34418	hypothetical prote	339	99	5.2	1772	2	A45532	major merzozite su
267	103.5	5.4	230	2	A56210	neu differentiation	340	99	5.2	2109	2	E89066	protein H05009.1 l
268	103.5	5.4	241	2	D43273	heregulin precursor	341	99	5.2	2109	2	T33247	hypothetical prote
269	103.5	5.4	270	2	A34636	FC-gamma receptor	342	99	5.2	416	2	A54017	colon carcinoma-as
270	103.5	5.4	636	2	I61718	neu differentiation	343	98.5	5.2	333	2	A31923	amalgam protein pr
271	103.5	5.4	637	2	C43273	heregulin precursor	344	98	5.1	421	2	T46266	hypothetical prote
272	103.5	5.4	639	2	I61719	neu differentiation	345	98	5.1	547	1	S28904	intercellular adhe
273	103.5	5.4	645	2	B43273	heregulin, splice	346	98	5.1	1535	2	S46224	peroxidasin - fru
274	103.5	5.4	662	2	I61722	neu differentiation	347	98	5.1	2541	2	T29340	hypothetical prote
275	103.5	5.4	1232	2	T43027	neural cell adhesi	348	97.5	5.1	272	2	I48268	biliary glycoprote
276	103.5	5.4	1375	2	T13822	frazzled gene prot	349	97.5	5.1	275	2	P90402	basigin type III -
277	103.5	5.4	1427	2	I51669	tumor suppressor -	350	97.5	5.1	793	2	D38992	protein-tyrosine k
278	103.5	5.4	1447	2	A54100	tumor suppressor p	351	97.5	5.1	976	1	TVHUKT	myosin-light-chain
279	103.5	5.4	1526	2	T13823	frazzled gene prot	352	97.5	5.1	413	2	S65948	hypothetical prote
280	103	5.4	372	2	C93971	Ig V-region-like B	353	97.5	5.1	414	2	C86301	hypothetical prote
281	103	5.4	569	2	A46462	T cell activation	354	97.5	5.1	535	2	T17212	cadherin 8 - human
282	103	5.4	680	2	JC5895	killer cell inhibi	355	97.5	5.1	793	2	D38992	protein-tyrosine k
283	103	5.4	739	2	J50675	vascular cell adhe	356	97.5	5.1	976	1	TVHUKT	myosin-light-chain
284	103	5.4	1259	2	S36126	neural cell adhesi	357	97.5	5.1	1147	2	A59307	hypothetical prote
285	103	5.4	1485	1	I82PT2	DNA topoisomerase	358	97.5	5.1	1520	2	T00273	hypothetical prote
286	102.5	5.4	426	2	S9016	pregnancy-specific	359	97	5.1	206	2	A40305	biliary glycoprote
287	102.5	5.4	429	1	E8HT	Ig epsilon chain C	360	97	5.1	274	2	T32736	hypothetical prote
288	102.5	5.4	1876	2	T28627	vitellinogenin - Rip	361	97	5.1	288	2	A55737	PD-1 protein - hum
289	102.5	5.4	6831	2	A88852	protein unc-22 (im	362	97	5.1	440	2	A43519	complement recept
290	102.5	5.4	6839	2	S57242	twitchin (similar	363	97	5.1	521	2	B63332	hypothetical prote
291	102.5	5.4	7160	2	T27935	hypothetical prote	364	97	5.1	572	2	B46529	Ig Y heavy chain (
292	102	5.3	324	2	G43354	pregnancy-specific	365	97	5.1	650	2	E82937	DNA topoisomerase,
293	102	5.3	326	2	F43354	pregnancy-specific	366	97	5.1	1026	1	A40315	maternal effect pr
294	102	5.3	333	2	A43354	pregnancy-specific	367	97	5.1	1177	2	T16594	hypothetical prote
295	102	5.3	527	2	T18232	conserved hypothet	368	97	5.1	1918	2	S43719	lactase (EC 3.2.1.
296	102	5.3	871	2	S47518	cadherin - African	369	97	5.1	1926	2	S01169	beta-glycosidase c
297	102	5.3	975	2	T30816	macrophage colony	370	96.5	5.1	246	1	A32999	myelin P0 protein
298	102	5.3	1089	2	T21582	hypothetical prote	371	96.5	5.1	332	2	JN0067	pregnancy-specific
299	101.5	5.3	226	2	A46477	membrane-bound imm	372	96.5	5.1	783	2	I50116	N-cadherin precurs
300	101.5	5.3	240	2	JG4121	pregnancy-specific	373	96.5	5.1	883	2	S57653	brevican precursor
301	101.5	5.3	402	2	A54312	pregnancy-specific	374	96.5	5.1	946	2	S28081	SCP1 protein - rat
302	101	5.3	344	2	T29264	hypothetical prote	375	96	5.0	370	2	S29139	aggregran - pig (fr
303	101	5.3	974	1	A49714	protein-tyrosine k	376	96	5.0	378	2	S61932	Ig V-region-like B
304	101	5.3	1176	2	JN0583	myosin-light-chain	377	96	5.0	398	2	A39371	Ig V-region-like B
305	101	5.3	1210	2	I39410	AF-4 protein, spli	378	96	5.0	662	2	T16525	hypothetical prote
306	101	5.3	1257	1	A41060	neural cell adhesi	379	96	5.0	769	1	ORRTGS	secretory componen
307	100.5	5.3	366	2	A53286	cell-surface glyco	380	96	5.0	857	2	S44883	ZC262.3 protein -
308	100.5	5.3	457	1	RWMS74	T-cell surface gly	381	96	5.0	1007	2	C84668	probable receptor
309	100.5	5.3	719	2	J30047	enhancer of split	382	96	5.0	1791	2	T02345	hypothetical prote
310	100.5	5.3	987	2	A88746	protein C18F3.2 [i	383	96	5.0	4930	2	E69679	polyketide synthet
311	100.5	5.3	1256	2	T03096	CD0 protein - rat	384	95.5	5.0	333	1	B42053	gap junction prote
312	100.5	5.3	1287	2	T30988	hypothetical prote	385	95.5	5.0	414	2	C75461	hypothetical prote
313	100	5.2	255	2	JC7593	SH2 domain-contain	386	95.5	5.0	451	2	S71754	cellular hepatitis
314	100	5.2	305	2	JC7593	nucleic acid-bindi	387	95.5	5.0	475	2	C86863	N-acetylmuramoyl-L
315	100	5.2	395	2	D43354	pregnancy-specific	388	95.5	5.0	583	2	J139428	alcam - human
316	100	5.2	397	2	D43354	pregnancy-specific	389	95.5	5.0	587	2	JH0464	DM-GRASP precursor
317	100	5.2	417	2	A28277	pregnancy-specific	390	95.5	5.0	647	2	JQ2149	B west mating prot
318	100	5.2	424	2	A34595	pregnancy-specific	391	95.5	5.0	811	2	PN0689	connectin 1 - chic
319	100	5.2	426	2	A35964	pregnancy-specific	392	95.5	5.0	993	2	S49481	synaptonemal compl
320	100	5.2	463	2	T29671	hypothetical prote	393	95	5.0	247	2	S58394	myelin/oligodendro
321	100	5.2	647	2	B41288	vascular cell adhe	394	95	5.0	271	2	S43512	GP42/basigin prote

395	95	5.0	273	2	JX0107	basigin precursor	468	91.5	4.8	267	2	A38442	probable tumor sup
396	95	5.0	435	2	D33258	pregnancy-specific	469	91.5	4.8	278	2	JC1506	biliary glycoprote
397	95	5.0	906	1	IHUCN	caderin 2 precurs	470	91.5	4.8	282	2	JC1507	biliary glycoprote
398	95	5.0	906	1	IHUCN	N-caderin precurs	471	91.5	4.8	430	2	I48142	B-lymphocyte anti
399	95	5.0	1106	1	PFHUGB	platelet-derived g	472	91.5	4.8	561	1	A44128	(N-acetylneuraminy
400	95	5.0	1248	2	B96827	hypothetical prote	473	91.5	4.8	1008	2	T41244	SEC14 protein homo
401	94.5	5.0	299	2	I46690	CD80 precursor - r	474	91.5	4.8	3507	2	T34513	hypothetical prote
402	94.5	5.0	353	1	VVVPB2	coat protein VP2 -	475	91	4.8	282	2	C28928	pregnancy-specific
403	94.5	5.0	451	2	T30603	perlecan homolog 2	476	91	4.8	304	2	G71624	rifin PF80025c - m
404	94.5	5.0	495	1	A26396	T-cell surface gly	477	91	4.8	336	2	I48471	Fc gamma (IgG) rec
405	94.5	5.0	503	2	S63257	probable membrane	478	91	4.8	344	2	T40167	hypothetical prote
406	94.5	5.0	547	2	T45635	hypothetical prote	479	91	4.8	401	1	QXBP1L	hypothetical prote
407	94.5	5.0	618	2	T08685	hypothetical prote	480	91	4.8	497	2	JC2054	complement regulat
408	94.5	5.0	757	2	S54620	RTS1 protein - yea	481	91	4.8	536	2	S71332	natriuretic peptid
409	94.5	5.0	905	1	IOXLC1	N-caderin 1 precu	482	91	4.8	810	2	G86797	prophage pi3 prote
410	94.5	5.0	1180	2	T20773	hypothetical prote	483	91	4.8	874	2	T29548	hypothetical prote
411	94.5	5.0	1260	1	S05479	neural cell adhesi	484	90.5	4.7	335	2	S58892	signaling lymphocy
412	94.5	5.0	1655	2	T32633	hypothetical prote	485	90.5	4.7	377	2	F71520	hypothetical prote
413	94.5	5.0	4549	2	T20771	hypothetical prote	486	90.5	4.7	404	2	A46480	Fc gamma (IgG) rec
414	94.5	5.0	4667	2	T20774	hypothetical prote	487	90.5	4.7	610	2	T44161	hypothetical prote
415	94	4.9	257	2	P80401	basigin type II -	488	90.5	4.7	964	2	S06028	gene suppressor-of
416	94	4.9	276	2	S20690	31.6K hypothetical	489	90.5	4.7	967	2	S66852	hypothetical prote
417	94	4.9	361	2	PN0020	fibroblast growth	490	90.5	4.7	1565	2	S04729	surface antigen pa
418	94	4.9	419	2	JC4123	pregnancy-specific	491	90.5	4.7	1882	1	GNVWTR	genome polyprotein
419	94	4.9	717	2	T22938	hypothetical prote	492	90.5	4.7	6805	2	S20901	titin - rabbit (fr
420	94	4.9	1227	2	T33004	hypothetical prote	493	90	4.7	142	2	S58082	transmembrane prot
421	94	4.9	1374	2	T330809	plasminogen relate	494	90	4.7	336	2	S42632	Fit-1S protein pre
422	94	4.9	1742	2	S24600	projectin - fruit	495	90	4.7	374	1	A39878	Fc gamma (IgG) rec
423	94	4.9	2124	2	A28452	proteoglycan core	496	90	4.7	464	2	C30127	transmembrane carc
424	94	4.9	3828	2	T13857	trithorax protein	497	90	4.7	556	2	S51892	probable membrane
425	93.5	4.9	243	2	A53244	leukocyte antigen	498	90	4.7	735	2	T15306	hypothetical prote
426	93.5	4.9	247	2	A55717	myelin P0 glycopro	499	90	4.7	882	2	I38912	receptor tyrosine k
427	93.5	4.9	249	1	A61087	myelin P0 glycopro	500	90	4.7	890	1	A53743	protein-tyrosine k
428	93.5	4.9	278	2	A39037	carcinoembryonic a	501	90	4.7	913	1	A47543	R-caderin precurs
429	93.5	4.9	355	2	B26883	neural cell adhesi	502	90	4.7	954	2	I51703	c-kit-related kina
430	93.5	4.9	466	2	JC5897	killer cell inhibi	503	90	4.7	962	2	T00262	hypothetical prote
431	93.5	4.9	535	2	A54155	natriuretic peptid	504	90	4.7	964	2	T15746	hypothetical prote
432	93.5	4.9	540	2	T44683	precocin methylas	505	90	4.7	1004	2	A55142	myosin-light-chain
433	93.5	4.9	2843	1	RHUPAP	adenomatous polyo	506	90	4.7	1029	2	T30351	integrin alpha-6 c
434	93	4.9	336	2	C27658	pregnancy-specific	507	90	4.7	1072	2	A38457	germline RNA helic
435	93	4.9	344	2	A41357	Fc gamma (IgG) rec	508	90	4.7	1156	2	T43326	hypothetical prote
436	93	4.9	769	2	B81447	chemotaxis histidi	509	90	4.7	1172	2	T32759	synapto-tyrosine k
437	93	4.9	773	1	ORRBG	secretory componen	510	90	4.7	1356	2	JC1402	vitellogenin, 170K
438	93	4.9	817	2	A48721	titin, muscle - ch	511	90	4.7	1575	2	S68448	synapto-tyrosine k
439	93	4.9	915	2	S74283	probable protein k	512	90	4.7	1659	2	JC4956	vitellogenin precu
440	93	4.9	976	1	TWNSMD	macrophage colony-	513	90	4.7	2090	2	S26058	probable transform
441	93	4.9	1840	2	T29091	transitin - chicke	514	90	4.7	13055	2	T16580	hypothetical prote
442	93	4.9	2132	1	A55182	aggreacan precursor	515	89.5	4.7	164	2	T16168	hypothetical prote
443	92.5	4.8	151	2	T21827	hypothetical prote	516	89.5	4.7	321	2	JH0395	biliary glycoprote
444	92.5	4.8	252	2	S33323	nonspecific cross-	517	89.5	4.7	335	2	A33514	pregnancy-specific
445	92.5	4.8	403	2	T27825	hypothetical prote	518	89.5	4.7	351	2	JH0396	biliary glycoprote
446	92.5	4.8	419	2	A36109	pregnancy-specific	519	89.5	4.7	416	2	S33473	interleukin-1 rece
447	92.5	4.8	628	2	I38000	Lutheran blood gro	520	89.5	4.7	417	2	JH0394	biliary glycoprote
448	92.5	4.8	757	2	I45956	polymeric immunogl	521	89.5	4.7	475	2	S45116	natriuretic peptid
449	92.5	4.8	829	2	A33166	colorectal tumor s	522	89.5	4.7	536	2	A45409	atrial natriuretic
450	92.5	4.8	1087	2	C84263	transmembrane olig	523	89.5	4.7	722	2	E71403	hypothetical prote
451	92.5	4.8	1114	2	I50222	deltaBPI - chicken	524	89.5	4.7	739	2	A41288	vascular cell adhe
452	92.5	4.8	1259	2	A34325	Bravo/Nr-CAM cell	525	89.5	4.7	757	1	S48841	secretory componen
453	92	4.8	238	2	S77699	inner cell wall ma	526	89.5	4.7	808	2	G83210	conserved hypotet
454	92	4.8	430	2	T28143	tapasin 1 homolog,	527	89.5	4.7	829	2	D71485	probable adenylate
455	92	4.8	511	2	S24345	Balbani ring 1 pr	528	89.5	4.7	1450	2	A44027	165K myofibrillar
456	92	4.8	688	2	T32750	hypothetical prote	529	89.5	4.7	1622	2	J80378	DNA (cytosine-5')-
457	92	4.8	1151	2	T18535	high molecular mas	530	89.5	4.7	2783	1	A41948	alpha-fetoprotein
458	92	4.8	1180	2	JC2132	metabotropic gluta	531	89.5	4.7	3924	2	S37431	ankyrin 2, neurona
459	92	4.8	1261	2	T13165	mutator 2 - fruit	532	89	4.7	245	2	A30154	IGF receptor alpha
460	92	4.8	1643	2	T14274	versican precursor	533	89	4.7	335	2	C54312	pregnancy-specific
461	92	4.8	1676	2	A56508	anucleate primary	534	89	4.7	335	2	B33251	nonspecific cross-
462	92	4.8	1807	2	S03124	vitellogenin A2 pr	535	89	4.7	432	2	S30193	T-cell surface gly
463	92	4.8	2397	1	A55535	versican precursor	536	89	4.7	475	2	S52893	hypothetical prote
464	92	4.8	2409	1	A60979	versican precursor	537	89	4.7	486	2	T51001	hypothetical prote
465	92	4.8	2415	1	A39086	aggreacan precursor	538	89	4.7	524	2	S35341	ketin - fruit fly
466	92	4.8	3036	2	T18995	hypothetical prote	539	89	4.7	565	2	T29718	hypothetical prote
467	92	4.8	3381	2	T42389	versican precursor	540	89	4.7	636	2	S63131	probable membrane

541	89	4.7	671	2	B54857	transcription fact	614	86.5	4.5	1125	2	B41206	microtubule-associ
542	89	4.7	1142	2	S59359	Gln4 protein - yea	615	86.5	4.5	1187	2	T19413	hypothetical prote
543	89	4.7	1560	2	S23727	proliferation pote	616	86.5	4.5	1327	2	T21268	hypothetical prote
544	89	4.7	1920	2	S43721	lactase (EC 3.2.1.1	617	86.5	4.5	1329	2	C69048	cobalamin biosynth
545	88.5	4.6	152	2	S21826	T-cell receptor be	618	86.5	4.5	1426	2	T30817	homeotic protein C
546	88.5	4.6	333	2	A40548	gap junction prote	619	86.5	4.5	1469	2	T19168	hypothetical prote
547	88.5	4.6	419	2	B54312	pregnancy-specific	620	86.5	4.5	1561	1	S06839	surface antigen ap
548	88.5	4.6	495	2	T25750	hypothetical prote	621	86.5	4.5	1659	2	H97926	hypothetical prote
549	88.5	4.6	519	2	H78089	G-protein signalin	622	86.5	4.5	1955	2	T30934	myosin-like protei
550	88.5	4.6	666	2	H89581	protein dim-1 [imp	623	86.5	4.5	2139	2	S46404	vitellogenin - yel
551	88.5	4.6	1213	2	B50198	serine/proline-ric	624	86.5	4.5	2327	2	T42630	aggregan - bovine
552	88.5	4.6	2233	2	A95075	beta-galactosidase	625	86.5	4.5	2944	2	A54849	collagen alpha 1(V
553	88.5	4.6	2845	2	T19505	adenomatous polypo	626	86	4.5	133	2	T46632	rearranged T-cell
554	88.5	4.6	3122	2	T17202	DNA-directed DNA p	627	86	4.5	366	2	I37135	MHC class I histoc
555	88.5	4.6	4436	2	E71086	hypothetical prote	628	86	4.5	448	1	VHIHBC	nucleocapsid prote
556	88	4.6	257	2	S00682	IGF FC receptor al	629	86	4.5	448	2	QJ1173	nucleocapsid prote
557	88	4.6	383	2	T46707	probable bacteriop	630	86	4.5	535	2	T37189	hypothetical prote
558	88	4.6	488	2	AG0621	conserved hypothet	631	86	4.5	537	1	A28111	natriuretic peptid
559	88	4.6	522	2	E89116	serine/threonine k	632	86	4.5	556	2	A44441	B-cell antigen CD1
560	88	4.6	856	2	T43631	N-cadherin precurs	633	86	4.5	648	2	A57284	spermatid perinocl
561	88	4.6	877	1	IJBOCN	unknown protein F5	634	86	4.5	712	2	T25438	hypothetical prote
562	88	4.6	884	2	D96730	metabotropic gluta	635	86	4.5	740	2	T09480	hypothetical prote
563	88	4.6	1212	2	JC2131	190K protein - hum	636	86	4.5	782	2	S50719	hypothetical prote
564	88	4.6	1451	2	S42167	vitellogenin - Ath	637	86	4.5	791	2	E35216	FRD5 protein - fow
565	88	4.6	1872	2	T30888	hypothetical prote	638	86	4.5	960	1	JN0677	protein-tyrosine k
566	87.5	4.6	400	2	T34363	hypothetical prote	639	86	4.5	1028	2	E24785	hypothetical prote
567	87.5	4.6	481	2	G81089	glucose-6-phosphat	640	86	4.5	1087	2	I51552	platelet-derived g
568	87.5	4.6	534	2	T39903	serine-rich protei	641	86	4.5	1124	2	JH0588	calmodulin-binding
569	87.5	4.6	644	2	G96748	hypothetical prote	642	86	4.5	1468	2	SL1515	formin - mouse
570	87.5	4.6	773	2	T46293	hypothetical prote	643	86	4.5	1852	1	VJCH2	vitellogenin II pr
571	87.5	4.6	834	2	S66438	M-sema F protein p	644	85.5	4.5	131	2	T20334	hypothetical prote
572	87.5	4.6	929	2	T38948	hypothetical colle	645	85.5	4.5	182	2	I83053	pregnancy-specific
573	87.5	4.6	937	2	S58135	hypothally regulated	646	85.5	4.5	307	2	D91602	infin PFB0955w - m
574	87.5	4.6	1087	2	T22847	hypothetical prote	647	85.5	4.5	321	2	D39371	Ig V-region-like B
575	87.5	4.6	1250	2	T22845	hypothetical prote	648	85.5	4.5	339	2	I56071	MHC class I histoc
576	87.5	4.6	1319	2	A28313	glued protein - fr	649	85.5	4.5	357	2	SL1139	class I histocompa
577	87.5	4.6	1436	2	S57238	forked protein 5.4	650	85.5	4.5	360	2	S69083	probable membrane
578	87.5	4.6	1449	2	S57237	forked protein 5.6	651	85.5	4.5	364	2	I46604	MHC PD14 transpla
579	87.5	4.6	1571	2	T00062	hypothetical prote	652	85.5	4.5	366	2	I46603	MHC PD14 transpla
580	87	4.6	233	2	JH0372	42K surface glycop	653	85.5	4.5	402	2	E86185	hypothetical prote
581	87	4.6	273	2	B28928	pregnancy-specific	654	85.5	4.5	457	1	A28468	chromogranin A pre
582	87	4.6	275	2	A28928	pregnancy-specific	655	85.5	4.5	671	2	A35912	homeotic protein o
583	87	4.6	391	2	T09058	butyrophilin homol	656	85.5	4.5	753	2	G02173	semaphorin III fam
584	87	4.6	408	2	S57148	hypothetical prote	657	85.5	4.5	796	2	T39962	coatamer complex b
585	87	4.6	422	2	S32357	glial growth facto	658	85.5	4.5	858	2	A57513	heat shock protein
586	87	4.6	431	2	S47538	acrosin (EC 3.4.21	659	85.5	4.5	929	2	T35683	fteK homolog - Str
587	87	4.6	448	1	VH1H1	nucleocapsid prote	660	85.5	4.5	1089	1	S33727	platelet-derived g
588	87	4.6	482	2	H86902	dextranucrase (EC	661	85.5	4.5	1151	2	T38424	hypothetical prote
589	87	4.6	838	2	I45537	eyeless, long form	662	85.5	4.5	1265	1	A37967	neural cell adhesi
590	87	4.6	874	2	B86332	FGA14.8 protein -	663	85.5	4.5	1315	2	T50262	probable nucleopor
591	87	4.6	939	2	S28394	probable serine/th	664	85.5	4.5	1324	2	S52863	DNA-binding protei
592	87	4.6	1032	2	G89437	protein T08P2.3 [i	665	85.5	4.5	1677	2	T43021	vitellogenin precu
593	87	4.6	1054	2	S54473	TPS3 protein - yea	666	85.5	4.5	2059	2	T13858	probable DNA-direc
594	87	4.6	1102	2	S55100	hypothetical prote	667	85.5	4.5	2094	2	S33124	tpx protein - huma
595	87	4.6	1118	1	A49724	protein-tyrosine-p	668	85.5	4.5	2271	2	F90073	hypothetical prote
596	87	4.6	1215	2	I52882	autoantigen - huma	669	85	4.5	191	2	C75011	hypothetical prote
597	87	4.6	1327	2	T09402	immunoglobulin-lik	670	85	4.5	246	2	A47712	myelin/oligodendro
598	87	4.6	1369	1	JC4860	protein-tyrosine k	671	85	4.5	267	2	A35902	Fc gamma (IgG) rec
599	87	4.6	1394	2	A29637	position-specific	672	85	4.5	324	2	I49768	bone sialoprotein
600	87	4.6	1465	2	S43529	155K protein, skel	673	85	4.5	392	2	H96338	membrane permease,
601	87	4.6	1603	2	SL7983	gene posterior sex	674	85	4.5	399	2	B64488	hypothetical prote
602	87	4.6	1823	2	S28974	vitellogenin precu	675	85	4.5	508	2	S12640	transposition prot
603	87	4.6	2491	1	A28372	insulin-like growt	676	85	4.5	528	2	PC4025	intercellular adhe
604	86.5	4.5	287	4	PC4402	peIB leader/Ig hea	677	85	4.5	625	2	T16777	hypothetical prote
605	86.5	4.5	459	2	A46254	CD4 precursor - ra	678	85	4.5	641	2	T17278	hypothetical prote
606	86.5	4.5	520	1	S44039	brain-derived neur	679	85	4.5	647	2	T23407	hypothetical prote
607	86.5	4.5	520	1	S44039	phosphoenolpyruvat	680	85	4.5	687	2	B87318	hypothetical prote
608	86.5	4.5	654	2	PC7085	nuclear factor of	681	85	4.5	712	2	T18195	gag protein - silk
609	86.5	4.5	677	2	T00369	hypothetical prote	682	85	4.5	728	2	T51071	related to trfA pr
610	86.5	4.5	818	1	S44038	brain-derived neur	683	85	4.5	779	2	T49717	related to BCS1 pr
611	86.5	4.5	906	1	IJXL22	N-cadherin 2 precu	684	85	4.5	1280	2	T29021	hypothetical prote
612	86.5	4.5	935	2	A40694	cadherin-associate	685	85	4.5	1370	2	T19188	hypothetical prote
613	86.5	4.5	976	2	T29583	hypothetical prote	686	85	4.5	1442	2	S72441	protein-tyrosine-p

687	85	4.5	1704	2	T43141	vitellogenin 1 - m	760	83	4.4	515	2	T05863	hypothetical prote
688	85	4.5	2500	1	WNUH22	HIV-EP2 enhancer-b	761	83	4.4	646	2	B84852	probable receptor-
689	84.5	4.4	212	2	C33258	pregnancy-specific	762	83	4.4	725	2	A41258	a-egglutin core
690	84.5	4.4	284	2	A35419	neutrophil protein	763	83	4.4	755	2	A12174	penicillin-binding
691	84.5	4.4	298	2	S57179	hypothetical prote	764	83	4.4	790	2	T22849	hypothetical prote
692	84.5	4.4	369	2	T497730	hypothetical prote	765	83	4.4	873	2	F96615	probable Myb-famil
693	84.5	4.4	381	2	S35940	class I histocompa	766	83	4.4	962	2	T04124	receptor-like prot
694	84.5	4.4	428	2	I57486	pregnancy-specific	767	83	4.4	1132	2	A35089	myosin-binding pro
695	84.5	4.4	428	2	JS00032	pregnancy-specific	768	83	4.4	1665	2	A48594	skeletin - mouse
696	84.5	4.4	458	1	RHUT4	T-cell surface gly	769	83	4.4	2232	2	T34434	hypothetical prote
697	84.5	4.4	460	2	B83552	probable two-compo	770	83	4.4	2630	2	T08868	polyprotein p1 - A
698	84.5	4.4	468	2	S44815	F44B9.4 protein -	771	82.5	4.3	238	2	C90909	probable major tai
699	84.5	4.4	508	2	H64223	pyruvate kinase (E	772	82.5	4.3	244	2	JC8019	CD58 protein - pig
700	84.5	4.4	567	2	T08405	hypothetical prote	773	82.5	4.3	286	2	S44835	F54HL2.3 protein -
701	84.5	4.4	604	2	S56027	hypothetical prote	774	82.5	4.3	347	2	AF3253	DNA-directed DNA p
702	84.5	4.4	611	1	EDBESM	hypothetical prote	775	82.5	4.3	357	2	AS4512	serine-repeat anti
703	84.5	4.4	783	2	F84514	immediate-early pr	776	82.5	4.3	380	2	T17236	hypothetical prote
704	84.5	4.4	889	2	T11742	hypothetical prote	777	82.5	4.3	448	1	A60003	nucleocapsid prote
705	84.5	4.4	897	2	T21688	egg sperm receptor	778	82.5	4.3	459	2	I48854	gene murine tumour
706	84.5	4.4	916	2	C28992	hypothetical prote	779	82.5	4.3	503	2	C84595	similar to pEARLI
707	84.5	4.4	1003	1	PRVZAM	cadherin 4 precurs	780	82.5	4.3	681	2	T00905	hypothetical prote
708	84.5	4.4	1089	1	PFHUGA	spheroidin precurs	781	82.5	4.3	709	2	A35364	carcinoembryonic a
709	84.5	4.4	1403	1	A47328	platelet-derived g	782	82.5	4.3	732	1	IJCHCB	B-cadherin precurs
710	84.5	4.4	1659	2	G95057	natural killer cel	783	82.5	4.3	736	2	G01522	acidic 82 kDa prot
711	84.5	4.4	1687	2	T43144	endo-beta-N-acetyl	784	82.5	4.3	767	2	S41479	DNA-binding protei
712	84.5	4.4	2172	2	T20145	vitellogenin II pr	785	82.5	4.3	785	2	S54016	SOK2 protein - yea
713	84	4.4	288	1	S28029	hypothetical prote	786	82.5	4.3	800	2	I51653	daRNA-binding prot
714	84	4.4	323	2	A48149	gene PD-1 protein	787	82.5	4.3	821	2	T19705	hypothetical prote
715	84	4.4	328	2	A38957	carcinoma-associat	788	82.5	4.3	850	2	JC5700	ERBB kinase activa
716	84	4.4	366	2	I81232	interleukin 12B pr	789	82.5	4.3	854	2	S02003	neurofilament trip
717	84	4.4	384	2	T41334	lymphocyte antigen	790	82.5	4.3	860	2	JC4566	chitinase (EC 3.2.
718	84	4.4	547	2	B45808	lan-like protein -	791	82.5	4.3	875	2	T33434	hypothetical prote
719	84	4.4	615	2	JC7576	B-lymphocyte antig	792	82.5	4.3	969	2	T03657	NAD ADP-riboethyla
720	84	4.4	621	2	A32838	transcription fact	793	82.5	4.3	989	2	AS4505	serine-repeat anti
721	84	4.4	708	2	T29669	DNA-directed RNA p	794	82.5	4.3	1063	2	D86731	hypothetical prote
722	84	4.4	742	2	A49672	hypothetical prote	795	82.5	4.3	1069	2	T00043	BH-protocadherin p
723	84	4.4	758	2	A29253	transcription fact	796	82.5	4.3	1072	2	T00041	BH-protocadherin p
724	84	4.4	760	2	S70294	finger protein hun	797	82.5	4.3	1088	1	PFRTGA	platelet-derived g
725	84	4.4	914	2	B48086	FUN21 protein - ye	798	82.5	4.3	1200	2	T00042	BH-protocadherin p
726	84	4.4	1037	2	E81980	translation initia	799	82.5	4.3	1205	2	T41987	hypothetical prote
727	84	4.4	1191	2	S76414	pilus-associated p	800	82.5	4.3	1335	2	T30211	hypothetical prote
728	84	4.4	1307	2	T30887	beta transducin-li	801	82.5	4.3	1365	2	S14871	interleukin-6 rece
729	84	4.4	1348	2	S16566	146D nuclear prote	802	82.5	4.3	1553	2	T03301	proline rich prote
730	84	4.4	1398	2	T25568	vascular endotheli	803	82.5	4.3	2282	2	T42717	hypothetical prote
731	84	4.4	1496	2	T19833	hypothetical prote	804	82.5	4.3	2517	2	S58380	probable RNA-direc
732	84	4.4	1507	2	B47328	hypothetical prote	805	82.5	4.3	182	2	A34647	pregnancy-specific
733	84	4.4	1609	2	S25345	natural killer cel	806	82	4.3	293	2	F75466	hypothetical prote
734	84	4.4	1670	2	S71551	probable membrane	807	82	4.3	320	1	GERTS	bone sialoprotein
735	84	4.4	3512	2	T17121	DNA-directed DNA p	808	82	4.3	339	2	T28138	Ig V-region-like B
736	83.5	4.4	309	2	S15674	CPV protein - midg	809	82	4.3	340	2	T28137	Ig V-region-like B
737	83.5	4.4	318	2	S32674	cell surface glyco	810	82	4.3	371	2	A53908	brevican precursor
738	83.5	4.4	390	2	T51201	K9R protein - vari	811	82	4.3	401	2	S53862	NADH2 dehydrogenas
739	83.5	4.4	403	2	I52590	hypothetical prote	812	82	4.3	416	2	F75434	hypothetical prote
740	83.5	4.4	478	2	AF3288	m33-B isoform - mo	813	82	4.3	468	1	A41242	interleukin-6 rece
741	83.5	4.4	488	2	A55180	pyruvate kinase (E	814	82	4.3	497	2	T41015	hypothetical prote
742	83.5	4.4	502	2	S36494	homeotic protein H	815	82	4.3	554	2	T25437	proline rich prote
743	83.5	4.4	528	2	I47141	E2 protein - human	816	82	4.3	579	2	D84137	hypothetical prote
744	83.5	4.4	580	2	T43481	gastric mucin (clo	817	82	4.3	623	2	T09306	methyl-accepting c
745	83.5	4.4	605	2	T43974	probable mucin DKP	818	82	4.3	646	2	JN0473	EFRF2 protein - hu
746	83.5	4.4	757	2	T34351	hypothetical prote	819	82	4.3	686	1	S28050	P-selectin precurs
747	83.5	4.4	913	2	S20590	hypothetical prote	820	82	4.3	752	2	T26508	transforming prote
748	83.5	4.4	942	2	D96814	exo-alpha-sialidas	821	82	4.3	776	2	A55448	hypothetical prote
749	83.5	4.4	1047	2	T46489	trehalose-6-phosph	822	82	4.3	798	2	T15336	hypothetical prote
750	83.5	4.4	1788	2	T1095	hypothetical prote	823	82	4.3	840	2	T01272	hypothetical prote
751	83	4.4	240	2	S01299	vitellogenin precu	824	82	4.3	846	2	A30889	integrin beta chai
752	83	4.4	265	2	A55811	OX-45 membrane gly	825	82	4.3	856	2	I58411	protein-tyrosine k
753	83	4.4	267	2	I56110	carcinoembryonic a	826	82	4.3	862	1	QRMSLD	hypothetical prote
754	83	4.4	288	2	B45580	Fc-gamma RIIB-als	827	82	4.3	919	2	T21663	projectin - fruit
755	83	4.4	343	2	T40306	transcription fact	828	82	4.3	940	2	A40985	hypothetical prote
756	83	4.4	349	2	A44507	hypothetical prote	829	82	4.3	1017	2	F82590	vgrG protein VCA01
757	83	4.4	352	2	T10905	adenylate cyclase	830	82	4.3	1086	2	JC6079	chitin synthase (E
758	83	4.4	365	2	I56053	class I histocompa	831	82	4.3	1162	2	PC4184	leptin receptor, O
759	83	4.4	393	2	S64303	cysteine synthase	832	82	4.3	1216	2	B90580	hypothetical prote

833	82	4.3	1589	2	T13606	hypothetical prote	906	81	4.2	1048	2	T30815	platelet-derived g
834	82	4.3	2761	2	T21064	hypothetical prote	907	81	4.2	1147	2	T35781	hypothetical prote
835	81.5	4.3	146	2	S26408	T-cell receptor be	908	81	4.2	1443	2	T31896	hypothetical prote
836	81.5	4.3	206	2	A39268	heterochromatin pr	909	81	4.2	1528	2	T06057	hypothetical prote
837	81.5	4.3	277	2	I52825	gene MAC25 protein	910	81	4.2	1684	2	JW0057	gravin - human
838	81.5	4.3	282	2	S50031	prostacyclin-stimu	911	81	4.2	1858	2	T18273	1-phosphatidylinos
839	81.5	4.3	282	2	T17219	hypothetical prote	912	81	4.2	2526	2	T20531	hypothetical prote
840	81.5	4.3	309	2	T15747	hypothetical prote	913	81	4.2	2722	2	T20532	hypothetical prote
841	81.5	4.3	341	2	A57136	class I histocompa	914	81	4.2	2738	2	T88320	protein F07A11.6 [
842	81.5	4.3	364	2	T46926	hypothetical prote	915	81	4.2	2738	2	T42730	Bassoon protein -
843	81.5	4.3	365	2	T35620	hypothetical prote	916	81	4.2	3942	2	T42730	Bassoon protein -
844	81.5	4.3	366	2	B37028	MHC class I histoc	917	80.5	4.2	5327	2	T13564	microtubule-associ
845	81.5	4.3	366	2	D52829	hypothetical prote	918	80.5	4.2	5327	2	S26266	T-cell receptor be
846	81.5	4.3	420	2	T14911	bZIP DNA-binding p	919	80.5	4.2	254	2	C42691	fibroblast growth
847	81.5	4.3	455	2	G01923	KIR (cl-5) NK rece	920	80.5	4.2	279	2	S53363	mucin 5AC (clone J
848	81.5	4.3	482	2	JC7583	basic helix-loop-h	921	80.5	4.2	299	2	T32982	hypothetical prote
849	81.5	4.3	498	2	S11246	LAG-3 protein prec	922	80.5	4.2	309	2	S19411	acetolactate synth
850	81.5	4.3	517	2	S20248	transcription fact	923	80.5	4.2	407	2	I52703	42K membrane glyco
851	81.5	4.3	567	2	S29498	lymphocyte antigen	924	80.5	4.2	468	2	B40228	neurexin I-beta pr
852	81.5	4.3	656	1	S59631	endo-1,4-beta-xyla	925	80.5	4.2	507	2	S05542	hypothetical prote
853	81.5	4.3	660	2	T02768	spike glycoprotein	926	80.5	4.2	523	2	C84753	hypothetical prote
854	81.5	4.3	661	2	T51779	non-phototropic hy	927	80.5	4.2	588	2	I37202	B-CAM protein - hu
855	81.5	4.3	699	2	A82425	helicase IV VCA071	928	80.5	4.2	598	2	A84616	hypothetical prote
856	81.5	4.3	735	2	A33369	glycogen(starch) s	929	80.5	4.2	642	2	B90767	probable terminase
857	81.5	4.3	767	2	T31558	hypothetical prote	930	80.5	4.2	642	2	G30970	probable terminase
858	81.5	4.3	818	2	T19120	hypothetical prote	931	80.5	4.2	654	2	A85717	hypothetical prote
859	81.5	4.3	829	1	I0HUCP	cadherin 3 precurs	932	80.5	4.2	658	2	S50831	endoglin precursor
860	81.5	4.3	860	2	JC5702	Erbb kinase activa	933	80.5	4.2	677	2	B69379	methy1-accepting c
861	81.5	4.3	868	2	JC5701	Erbb kinase activa	934	80.5	4.2	739	2	S18642	polynucleotide ade
862	81.5	4.3	876	2	I49152	protein-tyrosine k	935	80.5	4.2	906	2	JC5963	stable tubule only
863	81.5	4.3	880	2	B37433	protein-tyrosine k	936	80.5	4.2	917	2	I49639	glycoprotein 130 -
864	81.5	4.3	1027	2	A56733	chromatin remodel	937	80.5	4.2	926	2	B37271	A-alpha Y 3 protei
865	81.5	4.3	1032	2	S65341	probable membrane	938	80.5	4.2	971	1	A36376	replication licens
866	81.5	4.3	1054	2	D96519	myosin-like protei	939	80.5	4.2	1199	2	T23005	hypothetical prote
867	81.5	4.3	1184	2	T09484	cartilage intermed	940	80.5	4.2	1224	2	S28368	hypothetical prote
868	81.5	4.3	1201	2	A57369	anillin - fruit fl	941	80.5	4.2	1367	2	S51959	hypothetical prote
869	81.5	4.3	1205	2	S64819	probable membrane	942	80.5	4.2	1374	2	S69875	hypothetical prote
870	81.5	4.3	1417	2	H90670	probable invasin [	943	80.5	4.2	1460	2	D81675	polymorphic membra
871	81.5	4.3	1417	2	D85521	probable adhesin [	944	80.5	4.2	1461	2	T26327	hypothetical prote
872	81.5	4.3	1432	1	B36182	protein-tyrosine-p	945	80.5	4.2	1477	2	T13797	hypothetical prote
873	81.5	4.3	1530	2	I45944	neurexin I-alpha -	946	80.5	4.2	1507	2	A40228	neurexin I-alpha p
874	81.5	4.3	1621	2	T15264	hypothetical prote	947	80.5	4.2	1522	2	T39371	transcription regu
875	81.5	4.3	2453	2	S60254	nuclear receptor c	948	80.5	4.2	1547	2	T28657	blackjack protein,
876	81	4.2	138	2	D27639	T-cell receptor ga	949	80.5	4.2	1681	2	S59693	hypothetical prote
877	81	4.2	194	2	T39060	hypothetical prote	950	80.5	4.2	1859	2	S63325	probable membrane
878	81	4.2	253	2	T15475	hypothetical prote	951	80.5	4.2	1859	2	S64633	probable membrane
879	81	4.2	313	2	H36854	hemagglutinin - va	952	80.5	4.2	1862	2	I49502	ankyrin - mouse
880	81	4.2	351	2	G38196	hypothetical prote	953	80.5	4.2	2274	2	T30258	adenomatous polypo
881	81	4.2	351	2	AC3090	conserved hypothet	954	80	4.2	166	2	A33402	pregnancy-specific
882	81	4.2	354	2	I54551	histocompatibility	955	80	4.2	219	2	A11534	hypothetical prote
883	81	4.2	379	2	A81678	conserved hypothet	956	80	4.2	267	2	I72882	FC gamma receptor
884	81	4.2	414	2	A69907	cell wall-binding	957	80	4.2	313	2	JQ1862	31R protein - vari
885	81	4.2	426	2	B33580	neurexin III beta	958	80	4.2	351	2	S45305	CD44 antigen precu
886	81	4.2	509	2	JC5288	SHP substrate-1 pr	959	80	4.2	359	1	HLHU12	MHC class I histoc
887	81	4.2	513	2	JC5289	SHP substrate-1 pr	960	80	4.2	365	2	I38443	gene HLA-A-0203 pr
888	81	4.2	536	2	A40676	sphere organelle p	961	80	4.2	368	2	A45831	MHC class I histoc
889	81	4.2	551	2	S64314	probable membrane	962	80	4.2	406	2	S38170	SRP40 protein - ye
890	81	4.2	566	2	A49880	alpha-N-acetylglala	963	80	4.2	432	1	RWM074	T-cell surface gly
891	81	4.2	655	2	G56524	protein T1N15.9 li	964	80	4.2	432	1	AF3019	pyruvate kinase li
892	81	4.2	662	2	T18233	probable transcrip	965	80	4.2	479	2	C98255	pyruvate kinase (p
893	81	4.2	662	2	G94903	probable bHLH tran	966	80	4.2	499	2	A11472	heat-shock protein
894	81	4.2	769	2	T27550	hypothetical prote	967	80	4.2	539	2	F72288	methy1-accepting c
895	81	4.2	773	2	T00502	probable receptor-	968	80	4.2	550	2	T29919	hypothetical prote
896	81	4.2	808	1	T04982	dynamitin-like prote	969	80	4.2	573	2	A33533	cell surface glyco
897	81	4.2	873	2	JC7079	homeobox protein Z	970	80	4.2	584	2	B25682	homeotic protein E
898	81	4.2	883	2	S49126	breivican precursor	971	80	4.2	595	1	A48077	myb-related protei
899	81	4.2	895	2	S41225	leptin receptor, i	972	80	4.2	600	2	S07638	spore coat protein
900	81	4.2	919	2	A41275	DNA ligase (ATP) (	973	80	4.2	663	2	T37772	telomere length re
901	81	4.2	972	2	T49773	related to actin-i	974	80	4.2	732	2	C64972	probable ATPase -
902	81	4.2	972	2	F71608	hypothetical prote	975	80	4.2	743	2	B84639	probable ubiquitin
903	81	4.2	1016	2	T05066	hypothetical prote	976	80	4.2	772	2	A55004	transcription fact
904	81	4.2	1021	2	I39207	leukocyte surface	977	80	4.2	789	2	I50804	polyprotein - Japa
905	81	4.2	1046	2	T29776	hypothetical prote	978	80	4.2	791	2	A56241	aryl hydrocarbon r
							979	80	4.2	814	2	T26702	hypothetical prote

979	80	4.2	853	2	T46347	hypothetical prote	1052	79	4.1	792	2	S20554	pyruvate, water di
980	80	4.2	899	2	S51341	SGD1 protein - yea	1053	79	4.1	792	2	T29187	hypothetical prote
981	80	4.2	1143	2	T28129	hypothetical prote	1054	79	4.1	824	2	G81748	conserved hypothet
982	80	4.2	1194	2	C59436	KIAA1391 protein l	1055	79	4.1	825	1	EDBEXD	immediate-early pr
983	80	4.2	1257	2	S28764	neurocan precursor	1056	79	4.1	860	1	T06310	hypothetical prote
984	80	4.2	1471	2	B48218	neurexin III-alpha	1057	79	4.1	882	1	QRHULD	lbd receptor precu
985	80	4.2	2468	2	A83412	hypothetical prote	1058	79	4.1	883	2	S04722	puff 74E protein -
986	80	4.2	2588	2	T14342	NSD1 protein - mou	1059	79	4.1	912	2	A54423	brevican precursor
987	80	4.2	3432	1	GNWVUS	genome polyprotein	1060	79	4.1	948	2	A57640	retinoblastoma bin
988	79.5	4.2	132	1	RWMS12	T-cell receptor ga	1061	79	4.1	951	2	T26738	hypothetical prote
989	79.5	4.2	200	2	JC4357	HMGI protein - sea	1062	79	4.1	971	2	B90835	probable tail fibe
990	79.5	4.2	213	2	S35522	heterochromatin pr	1063	79	4.1	973	2	C85693	neural kinesin h
991	79.5	4.2	218	2	JC7220	nuclear protein SR	1064	79	4.1	1032	2	I38510	hypothetical prote
992	79.5	4.2	299	2	T12483	hypothetical prote	1065	79	4.1	1038	2	S52522	hypothetical prote
993	79.5	4.2	303	2	H83108	hypothetical prote	1066	79	4.1	1098	1	PFMSRB	platelet-derived g
994	79.5	4.2	392	2	T46418	hypothetical prote	1067	79	4.1	1098	2	T08599	probable transcrip
995	79.5	4.2	423	2	A84483	probable protein k	1068	79	4.1	1122	2	G64887	probable tail fibe
996	79.5	4.2	425	2	E71276	hypothetical prote	1069	79	4.1	1169	2	T30207	dysnein heavy chain
997	79.5	4.2	426	2	JH0518	lymphocyte homing	1070	79	4.1	1263	2	T15496	hypothetical prote
998	79.5	4.2	475	2	A54879	pregnancy-specific	1071	79	4.1	1310	1	WZBE62	gene 62 protein -
999	79.5	4.2	577	2	T48530	clathrin binding p	1072	79	4.1	1367	1	S48478	glucan 1,4-alpha-g
1000	79.5	4.2	640	1	S76024	conserved hypothet	1073	79	4.1	1418	2	T15232	hypothetical prote
1001	79.5	4.2	646	2	T02398	hypothetical prote	1074	79	4.1	1461	2	E90696	hypothetical prote
1002	79.5	4.2	658	2	S68418	protein phosphatas	1075	79	4.1	1461	2	A85547	hypothetical prote
1003	79.5	4.2	680	2	T30620	hypothetical prote	1076	79	4.1	1994	2	D86452	protein F6N18.13 l
1004	79.5	4.2	688	2	A83179	conserved hypothet	1077	79	4.1	2109	1	I50421	aggreccan precursor
1005	79.5	4.2	697	2	T16908	hypothetical prote	1078	79	4.1	4543	1	A53102	alpha-2-macroglobu
1006	79.5	4.2	736	2	T41259	hypothetical prote	1079	79	4.1	4544	1	S02352	alpha-2-macroglobu
1007	79.5	4.2	819	2	A47018	lectin-like adhesi	1080	79	4.1	4545	1	S25111	gp330 protein prec
1008	79.5	4.2	831	2	T49721	hypothetical prote	1081	79	4.1	4660	2	T42737	Ig heavy chain V r
1009	79.5	4.2	837	2	A00159	outer membrane ush	1082	78.5	4.1	115	2	S19968	T-cell surface gly
1010	79.5	4.2	861	1	VCLJSC	env polyprotein pr	1083	78.5	4.1	246	2	A29523	protein F58A4.1 li
1011	79.5	4.2	909	2	H86350	hypothetical prote	1084	78.5	4.1	254	2	D98550	B16r protein - vac
1012	79.5	4.2	982	2	A32523	microtubule-associ	1085	78.5	4.1	290	2	F42527	hypothetical prote
1013	79.5	4.2	1018	2	S44758	CL1489.6 protein -	1086	78.5	4.1	301	2	G85928	hypothetical prote
1014	79.5	4.2	1032	2	T34433	hypothetical prote	1087	78.5	4.1	303	2	S40973	hypothetical prote
1015	79.5	4.2	1033	2	A96714	hypothetical prote	1088	78.5	4.1	334	2	E86794	probable G-box bin
1016	79.5	4.2	1051	2	T51904	hypothetical prote	1089	78.5	4.1	346	2	H85057	probable G-box bin
1017	79.5	4.2	1139	1	S61918	protein kinase C (	1090	78.5	4.1	360	2	T03373	hypothetical prote
1018	79.5	4.2	1152	2	A33183	microtubule-associ	1091	78.5	4.1	362	2	B40784	hypothetical prote
1019	79.5	4.2	1163	2	I56126	lymphocyte fuction	1092	78.5	4.1	366	2	S42823	MHC class I histoc
1020	79.5	4.2	1269	2	S35366	furin (EC 3.4.21.7	1093	78.5	4.1	420	2	T46910	hypothetical prote
1021	79.5	4.2	1274	2	S55050	cardiac myosin-bin	1094	78.5	4.1	445	2	T42203	serotonin receptor
1022	79.5	4.2	1311	2	G86471	unknown protein li	1095	78.5	4.1	457	2	S03961	Ig mu chain C regi
1023	79.5	4.2	1311	2	T08986	hypothetical prote	1096	78.5	4.1	494	2	A48133	pre-mRNA splicing
1024	79.5	4.2	1392	2	T18314	hypothetical prote	1097	78.5	4.1	560	2	T40608	conserved hypothet
1025	79.5	4.2	3005	2	S33642	homeotic protein z	1098	78.5	4.1	574	2	C86400	hypothetical prote
1026	79.5	4.2	6713	2	B89921	hypothetical prote	1099	78.5	4.1	605	2	S48940	hypothetical prote
1027	79	4.1	218	2	JC4788	sodium channel pro	1100	78.5	4.1	627	2	T27123	hypothetical prote
1028	79	4.1	238	2	I68699	MHC HLA-A cell sur	1101	78.5	4.1	723	2	T14765	hypothetical prote
1029	79	4.1	250	2	A34342	IgE Fc receptor al	1102	78.5	4.1	748	2	T51738	RNA helicase RH3 l
1030	79	4.1	264	2	I46020	FC gamma 2 recepto	1103	78.5	4.1	869	2	A36558	probable protein k
1031	79	4.1	268	2	T23555	hypothetical prote	1104	78.5	4.1	894	2	S25332	hypothetical prote
1032	79	4.1	270	2	B75581	probable cytochrom	1105	78.5	4.1	892	2	S25332	interleukin-6 sign
1033	79	4.1	315	2	H35216	FP31 protein - fow	1106	78.5	4.1	918	2	A44257	flagellum-associat
1034	79	4.1	316	1	QRHUT2	microtubule-associ	1107	78.5	4.1	959	2	S32016	modification methy
1035	79	4.1	326	2	T37450	interleukin-1 beta	1108	78.5	4.1	969	2	H69425	ionotropic glutama
1036	79	4.1	338	2	A39953	MHC class I histoc	1109	78.5	4.1	976	2	T51137	hypothetical prote
1037	79	4.1	363	1	S42102	probable membrane	1110	78.5	4.1	1012	2	T24384	hsdr protein - kie
1038	79	4.1	368	2	H96990	microtubule-associ	1111	78.5	4.1	1013	2	T30818	Ap-3 adaptor compl
1039	79	4.1	441	1	QRHUT1	cell wall-binding	1112	78.5	4.1	1105	2	T18295	hypothetical prote
1040	79	4.1	461	2	H84099	glucose-6-phosphat	1113	78.5	4.1	1196	2	H86389	DNA-directed RNA p
1041	79	4.1	481	2	E81854	hypothetical prote	1114	78.5	4.1	1224	2	S73171	protein-tyrosine k
1042	79	4.1	482	2	T22981	hypothetical prote	1115	78.5	4.1	1235	2	T13710	Ras guanine nucleo
1043	79	4.1	484	2	S66713	conserved hypothet	1116	78.5	4.1	1333	2	A37488	atypical protein k
1044	79	4.1	488	2	AD0735	hypothetical prote	1117	78.5	4.1	1337	2	T13948	hypothetical prote
1045	79	4.1	528	2	T34941	probable Na+/H+ an	1118	78.5	4.1	1358	2	B86241	hypothetical prote
1046	79	4.1	542	2	S64030	probable membrane	1119	78.5	4.1	1382	2	S70310	protein-tyrosine k
1047	79	4.1	586	2	C30411	synapsin Ila - rat	1120	78.5	4.1	1386	2	T49316	genome polyprotein
1048	79	4.1	610	2	T06280	probable starch sy	1121	78.5	4.1	1440	1	GNWVUF	saliva-interacting
1049	79	4.1	615	2	T39758	proline-serine ric	1122	78.5	4.1	1556	2	A60988	peroxisome prolife
1050	79	4.1	741	2	I51657	suppressor of yea	1123	78.5	4.1	1560	2	T02885	protein-tyrosine-p
1051	79	4.1	792	2	A90930	phosphoenolpyruvat	1124	78.5	4.1	1615	2	B49502	



1125	78.5	4.1	1736	2	F86178	hypothetical prote	1198	77.5	4.1	353	2	B53250	class I histocompa
1126	78.5	4.1	1766	2	A42125	trophozoite cystei	1199	77.5	4.1	354	2	I69002	histocompatibility
1127	78.5	4.1	1767	2	A49502	protein-tyrosine-p	1200	77.5	4.1	361	2	B59099	hypothetical prote
1128	78.5	4.1	1777	2	T34369	hypothetical prote	1201	77.5	4.1	364	1	S31304	protein-tyrosine-p
1129	78.5	4.1	1796	2	S65004	probable membrane	1202	77.5	4.1	364	1	A35997	MHC class I histoc
1130	78.5	4.1	1911	2	T43048	calcium channel al	1203	77.5	4.1	365	2	I37483	HLA-A*34.2 antigen
1131	78.5	4.1	1977	2	S54771	sodium channel alp	1204	77.5	4.1	366	2	A60369	MHC class I histoc
1132	78.5	4.1	1997	1	S12050	protein-tyrosine-p	1205	77.5	4.1	401	2	A57226	mel-S332 protein -
1133	78.5	4.1	2055	2	T00093	hypothetical prote	1206	77.5	4.1	402	1	QBOT2	microtubule-associ
1134	78.5	4.1	2559	2	T09144	probable guanine n	1207	77.5	4.1	440	2	S74969	hypothetical prote
1135	78.5	4.1	3078	2	T28432	variant-specific s	1208	77.5	4.1	450	2	T25542	hypothetical prote
1136	78	4.1	214	2	D96839	F23A5.5 [imported]	1209	77.5	4.1	454	1	MHHY	Ig mu chain C regi
1137	78	4.1	218	2	A55734	sodium channel, vo	1210	77.5	4.1	457	2	S73774	diacylglycerol
1138	78	4.1	218	2	A42737	hypothetical prote	1211	77.5	4.1	460	2	T45968	hypothetical prote
1139	78	4.1	286	2	C84877	hypothetical prote	1212	77.5	4.1	474	2	T00699	hypothetical prote
1140	78	4.1	317	2	T39869	probable lysophosp	1213	77.5	4.1	474	2	AG2269	heterocyst specif
1141	78	4.1	332	2	H82064	conserved hypothet	1214	77.5	4.1	486	2	D70154	replication initia
1142	78	4.1	349	2	T41394	hypothetical serin	1215	77.5	4.1	495	1	FWSYG2	glycinin chain Ala
1143	78	4.1	357	2	S11133	class I histocompa	1216	77.5	4.1	499	2	T45749	hypothetical prote
1144	78	4.1	366	2	I37078	HLA-C alpha chain	1217	77.5	4.1	500	2	B44055	envelope protein -
1145	78	4.1	371	2	E84709	hypothetical prote	1218	77.5	4.1	500	2	A44055	envelope protein -
1146	78	4.1	391	2	T36321	hypothetical prote	1219	77.5	4.1	531	2	T18931	hypothetical prote
1147	78	4.1	469	2	S76891	hypothetical prote	1220	77.5	4.1	537	2	I49769	intercellular adhe
1148	78	4.1	481	2	A27626	sucrose phosphoryl	1221	77.5	4.1	537	2	A45815	interleukin 1 recep
1149	78	4.1	487	1	BWSOGM	gtfa protein - Str	1222	77.5	4.1	570	2	A57535	myb-related protei
1150	78	4.1	504	2	I56542	calmodulin-binding	1223	77.5	4.1	590	1	S55095	myb-related protei
1151	78	4.1	511	2	A97212	protein containing	1224	77.5	4.1	594	1	D55514	diacylglycerol
1152	78	4.1	513	2	T34546	hypothetical prote	1225	77.5	4.1	625	2	T41603	alpha-amylase - fi
1153	78	4.1	517	2	T40129	hypothetical prote	1226	77.5	4.1	630	2	I51086	prolactin receptor
1154	78	4.1	536	2	T37544	hypothetical serin	1227	77.5	4.1	642	2	B49849	terminase large ch
1155	78	4.1	540	2	T00646	hypothetical prote	1228	77.5	4.1	646	1	S15901	chromogranin B pre
1156	78	4.1	551	1	S52667	seed biotin-contai	1229	77.5	4.1	665	1	H97093	fructose-bisphosph
1157	78	4.1	555	2	J01526	interleukin-1 rece	1230	77.5	4.1	716	2	T19355	hypothetical prote
1158	78	4.1	564	2	I53106	gene gli protein -	1231	77.5	4.1	722	2	B86583	transcription elon
1159	78	4.1	574	2	A84782	hypothetical prote	1232	77.5	4.1	722	2	C72040	transcription elon
1160	78	4.1	577	2	S64613	probable membrane	1233	77.5	4.1	735	2	T45059	hypothetical prote
1161	78	4.1	621	2	T24090	hypothetical prote	1234	77.5	4.1	888	2	S23065	ufo protein - mous
1162	78	4.1	660	2	JW0067	chitinase (EC 3.2.	1235	77.5	4.1	921	2	AE0332	conserved hypothet
1163	78	4.1	671	2	T12976	hypothetical prote	1236	77.5	4.1	940	2	S19702	fibronectin-bindin
1164	78	4.1	682	2	T43292	G protein-linked a	1237	77.5	4.1	1054	2	T30901	cyclic nucleotide
1165	78	4.1	713	2	A95942	probable bifunctio	1238	77.5	4.1	1130	2	A48843	MHC class II trans
1166	78	4.1	739	2	JN0581	vascular cell adhe	1239	77.5	4.1	1293	2	S24202	xeroderma pigmento
1167	78	4.1	753	2	F93338	pyruvate, water di	1240	77.5	4.1	1495	2	S60255	transcription co-r
1168	78	4.1	763	2	T24367	hypothetical prote	1241	77.5	4.1	2048	2	AG2109	hypothetical prote
1169	78	4.1	765	2	T49592	neurofilament trip	1242	77.5	4.1	2109	2	I38414	transcription fact
1170	78	4.1	785	2	I50180	cadherin-7 - chick	1243	77.5	4.1	2470	2	I50726	cation-independent
1171	78	4.1	792	2	E85778	phosphoenolpyruvat	1244	77.5	4.1	3212	2	T24692	hypothetical prote
1172	78	4.1	831	2	T49758	related to cytochr	1245	77	4.0	162	2	I51688	tumor suppressor -
1173	78	4.1	841	1	I78885	serine/threonine-s	1246	77	4.0	186	2	I61783	sodium channel bet
1174	78	4.1	915	2	T09575	smoothelin - human	1247	77	4.0	203	2	C87801	protein C10G11.9 [
1175	78	4.1	919	2	T32541	unc-5 protein - Ca	1248	77	4.0	203	2	T25916	hypothetical prote
1176	78	4.1	941	2	T51135	ligand-gated chann	1249	77	4.0	214	2	H96842	F23A5.34 [imported
1177	78	4.1	942	2	S23251	protein-tyrosine k	1250	77	4.0	287	2	B96717	unknown protein, 3
1178	78	4.1	947	1	B44294	unc-5 protein, lon	1251	77	4.0	316	2	C37028	MHC class I histoc
1179	78	4.1	966	2	S25365	Cyc8 protein - yea	1252	77	4.0	326	2	JC4124	pregnancy-specific
1180	78	4.1	1038	2	H90053	hypothetical prote	1253	77	4.0	357	2	S11137	class I histocompa
1181	78	4.1	1047	2	A59246	HIRA protein - fru	1254	77	4.0	364	2	I72217	class I histocompa
1182	78	4.1	1095	2	T20528	hypothetical prote	1255	77	4.0	365	2	I61902	MHC class I histoc
1183	78	4.1	1137	2	JC5950	integrin alpha-7 c	1256	77	4.0	393	2	S63379	probable membrane
1184	78	4.1	1158	2	S73348	nuclear factor RIF	1257	77	4.0	432	1	RWC274	T-cell surface gly
1185	78	4.1	1174	2	A40853	potassium channel	1258	77	4.0	435	2	S75346	hypothetical prote
1186	78	4.1	1191	2	T14154	serine/threonine p	1259	77	4.0	450	2	AD1710	phosphoglucosidase
1187	78	4.1	1289	2	T31344	GP80 precursor - s	1260	77	4.0	452	2	T40769	hypothetical prote
1188	78	4.1	1389	2	T03273	embryogenesis tran	1261	77	4.0	484	2	T25731	hypothetical prote
1189	78	4.1	1650	2	S53457	dominant autoantig	1262	77	4.0	511	2	T23189	hypothetical prote
1190	78	4.1	2165	2	T21371	hypothetical prote	1263	77	4.0	521	2	T21440	hypothetical prote
1191	78	4.1	2238	1	ZLNZSV	genome polyprotein	1264	77	4.0	527	2	F89240	protein K01D12.6 [
1192	78	4.1	2928	2	T14261	Bassoon protein -	1265	77	4.0	530	2	S46589	UTR1 protein - yea
1193	78	4.1	5170	2	T15348	hypothetical prote	1266	77	4.0	571	2	A11094	probable peptidogl
1194	77.5	4.1	202	2	A42410	hydocan precursor	1267	77	4.0	607	2	C75432	dihydroxy-acid deh
1195	77.5	4.1	214	2	B97143	hypothetical secre	1268	77	4.0	644	2	S39356	transcription fact
1196	77.5	4.1	319	2	E96715	protein F4N2.12 [i	1269	77	4.0	646	2	JQ2150	B west mating prot
1197	77.5	4.1	345	2	T29786	hypothetical prote	1270	77	4.0	662	2	D40228	neurexin II-beta p

1271	77	4.0	721	2	F82198	probable toxin sec	1344	76.5	4.0	1466	2	T32422	hypothetical prote
1272	77	4.0	810	2	S69652	hypothetical prote	1345	76.5	4.0	1567	2	T03730	antigen containing
1273	77	4.0	875	2	S62177	Hir2 protein - yea	1346	76.5	4.0	1679	2	S49802	probable membrane
1274	77	4.0	884	2	S77031	hypothetical prote	1347	76.5	4.0	2228	2	E97942	beta-galactosidase
1275	77	4.0	886	2	S29605	glycoprotein 350/2	1348	76.5	4.0	2488	2	T42739	guanine nucleotide
1276	77	4.0	887	2	T20941	hypothetical prote	1349	76.5	4.0	3432	1	GNWJJE	genome polyprotein
1277	77	4.0	913	1	IJCHCR	R-cadherin precurs	1350	76	4.0	198	2	JC1457	myelin/oligodendro
1278	77	4.0	920	2	T22426	dynamlin-like prote	1351	76	4.0	218	2	B47712	ryudocan precursor
1279	77	4.0	940	2	T01854	hypothetical prote	1352	76	4.0	235	2	168700	MHC HLA-A cell sur
1280	77	4.0	947	2	T02512	hypothetical prote	1353	76	4.0	247	2	S74912	hypothetical prote
1281	77	4.0	1023	2	G82213	hypothetical prote	1354	76	4.0	267	2	T52381	hypothetical prote
1282	77	4.0	1048	2	H87721	protein ZC123.2 [i	1355	76	4.0	273	2	F91083	hypothetical prote
1283	77	4.0	1095	2	T43275	neurabin - rat	1356	76	4.0	283	2	T11644	hypothetical prote
1284	77	4.0	1106	2	S38783	integrin alpha cha	1357	76	4.0	313	2	E70951	hypothetical prote
1285	77	4.0	1199	2	T29145	hypothetical prote	1358	76	4.0	318	2	D71441	class I histocompa
1286	77	4.0	1518	2	S37928	probable purine nu	1359	76	4.0	329	2	A40730	probable secreted
1287	77	4.0	1534	2	A85862	hypothetical prote	1360	76	4.0	331	2	T35100	hypothetical prote
1288	77	4.0	1534	2	G91017	probable membrane	1361	76	4.0	336	2	T30757	MHC class I histoc
1289	77	4.0	1549	2	T21809	hypothetical prote	1362	76	4.0	348	2	150107	class I histocompa
1290	77	4.0	1715	2	C40228	neurexin II-alpha	1363	76	4.0	355	2	B40730	class I histocompa
1291	77	4.0	1812	2	I49350	breast/ovarian can	1364	76	4.0	356	2	A27797	translation releas
1292	77	4.0	1912	2	T37088	vitellogenin I pre	1365	76	4.0	356	2	JH0289	HLA-A*0210 - hum
1293	77	4.0	2237	2	T45115	N-type calcium cha	1366	76	4.0	361	2	B82533	hypothetical prote
1294	77	4.0	3562	2	A47171	chondroitin sulfat	1367	76	4.0	365	2	T37470	homeotic protein H
1295	76.5	4.0	116	2	C27390	Ig lambda chain pr	1368	76	4.0	403	2	T49603	hypothetical prote
1296	76.5	4.0	127	2	T30102	hypothetical prote	1369	76	4.0	409	2	A39621	hypothetical prote
1297	76.5	4.0	139	2	C27639	T-cell receptor ga	1370	76	4.0	476	2	T25147	hypothetical prote
1298	76.5	4.0	202	2	I53137	fibroglycan (synde	1371	76	4.0	490	2	T26067	actin-like protein
1299	76.5	4.0	235	2	S20000	Ig light chain pre	1372	76	4.0	500	2	T37488	hypothetical prote
1300	76.5	4.0	237	2	T13649	hypothetical prote	1373	76	4.0	523	2	S66148	gene pipsaqueak pr
1301	76.5	4.0	242	2	T48519	hypothetical prote	1374	76	4.0	535	2	A75481	sensor histidine k
1302	76.5	4.0	274	2	S71527	outer surface prot	1375	76	4.0	566	2	A75481	AP-9 protein - hum
1303	76.5	4.0	302	2	C36464	fibroblast growth	1376	76	4.0	568	2	T39411	hypothetical prote
1304	76.5	4.0	325	2	S46760	hypothetical prote	1377	76	4.0	602	2	B22313	hypothetical prote
1305	76.5	4.0	341	2	AC1507	hypothetical prote	1378	76	4.0	616	2	T32753	hypothetical prote
1306	76.5	4.0	359	2	S24240	lymphocyte surface	1379	76	4.0	635	2	F75477	endoglin precursor
1307	76.5	4.0	363	2	T47588	hypothetical prote	1380	76	4.0	640	1	QOBEU2	Urf35 protein - hum
1308	76.5	4.0	380	2	G96904	spore coat protein	1381	76	4.0	653	2	A49722	hypothetical prote
1309	76.5	4.0	400	2	S52733	hypothetical prote	1382	76	4.0	655	2	T28885	probable gtpase ac
1310	76.5	4.0	445	2	AF0033	H+-transporting tw	1383	76	4.0	670	2	E86184	nucleolus-cycoplas
1311	76.5	4.0	474	1	ONHUIB	alpha-1-B-glycopro	1384	76	4.0	695	2	T39954	splicing regulator
1312	76.5	4.0	475	2	I76668	pregnancy-specific	1385	76	4.0	734	2	B42680	Balbani ring 2.1
1313	76.5	4.0	493	2	S13530	CD4E protein, epi	1386	76	4.0	749	2	S50095	hypothetical prote
1314	76.5	4.0	497	2	S47890	exuperantia 1 - fr	1387	76	4.0	757	2	T05688	hypothetical prote
1315	76.5	4.0	500	2	B98260	hypothetical prote	1388	76	4.0	775	1	EDBE11	immediate-early pr
1316	76.5	4.0	500	2	AG3024	histidase hucH [im	1389	76	4.0	776	2	T33543	hypothetical prote
1317	76.5	4.0	508	2	A29605	protein A precurs	1390	76	4.0	822	2	T51049	related to nucleol
1318	76.5	4.0	523	2	S67271	hypothetical prote	1391	76	4.0	839	2	F75518	hypothetical prote
1319	76.5	4.0	539	2	S47143	A nating type prot	1392	76	4.0	853	2	A71339	probable outer mem
1320	76.5	4.0	539	2	B72707	hypothetical prote	1393	76	4.0	860	2	F71000	hypothetical prote
1321	76.5	4.0	545	2	JU0341	intercellular adhe	1394	76	4.0	887	1	IUCHCL	E-cadherin precurs
1322	76.5	4.0	602	2	A45769	acetylcholine rece	1395	76	4.0	944	2	H64650	translation initia
1323	76.5	4.0	607	2	A43776	drebrin E2 - chick	1396	76	4.0	960	2	T17297	hypothetical prote
1324	76.5	4.0	690	2	I51298	transforming prote	1397	76	4.0	966	2	S43878	trwC protein - Esc
1325	76.5	4.0	709	2	C28821	1-phosphatidylinos	1398	76	4.0	995	2	S50358	hypothetical prote
1326	76.5	4.0	761	2	T26955	hypothetical prote	1399	76	4.0	1002	2	T09438	toxR-activated lip
1327	76.5	4.0	786	2	T16509	hypothetical prote	1400	76	4.0	1013	2	B82276	toxR-activated gen
1328	76.5	4.0	789	2	C83949	hypothetical prote	1401	76	4.0	1029	2	T02576	hypothetical prote
1329	76.5	4.0	812	2	A81096	cell division prot	1402	76	4.0	1054	2	T43226	translation initia
1330	76.5	4.0	815	2	T45744	probable ubiquitin	1403	76	4.0	1057	2	H83273	ribonuclease E PA2
1331	76.5	4.0	865	2	T46651	transcription acti	1404	76	4.0	1085	2	S66149	gene pipsaqueak pr
1332	76.5	4.0	891	2	A46203	mating type A-alph	1405	76	4.0	1192	2	T18611	probable serine/th
1333	76.5	4.0	896	2	S48761	trehalose-phosphat	1406	76	4.0	1230	2	T18259	serine/threonine p
1334	76.5	4.0	899	2	A35895	androgen receptor	1407	76	4.0	1237	2	A34598	ecdysone-induced p
1335	76.5	4.0	928	2	B71617	protein F55C7.7c [	1408	76	4.0	1280	2	T00365	hypothetical prote
1336	76.5	4.0	987	2	A87749	SERA antigen/papal	1409	76	4.0	1355	2	S40022	spalt protein - fr
1337	76.5	4.0	997	2	B71617	atrophin-1 - human	1410	76	4.0	1357	2	T29265	hypothetical prote
1338	76.5	4.0	1184	2	S50832	atrophin-1 - human	1411	76	4.0	1374	2	D72593	hypothetical prote
1339	76.5	4.0	1184	2	G01763	protein ZK250.10 [	1412	76	4.0	1394	2	B34598	ecdysone-induced p
1340	76.5	4.0	1192	2	F88062	hypothetical prote	1413	76	4.0	1403	2	T11583	probable translati
1341	76.5	4.0	1234	2	T31623	neurocan - mouse	1414	76	4.0	1457	2	D81019	adhesion and penet
1342	76.5	4.0	1268	2	S52781	neural specific DN	1415	76	4.0	1578	2	I48216	neurexin III-alpha
1343	76.5	4.0	1361	2	T30884	F7H2.12 protein -	1416	76	4.0				
1344	76.5	4.0	1366	2	B86292								

1417 76 4.0 1679 2 T30271 surface protein -  
1418 76 4.0 1726 2 T30810 chromatin structur  
1419 76 4.0 1737 2 A59235 nonconventional myo  
1420 76 4.0 1804 2 T34518 nestin - golden ha  
1421 76 4.0 1810 1 A32230 tenascin precursor  
1422 76 4.0 1931 2 A59234 slow myosin heavy  
1423 76 4.0 2124 2 A59234 hypothetical prote  
1424 76 4.0 2167 2 A1489 cell wall-associat  
1425 76 4.0 2624 2 T16870 hypothetical prote  
1426 76 4.0 3624 2 A80835 large repetitive p  
1427 76 4.0 4006 2 T09070 probable tenascin  
1428 75.5 4.0 102 2 C32530 Ig heavy chain v r  
1429 75.5 4.0 116 2 S22553 Ig heavy chain v r  
1430 75.5 4.0 131 2 A27472 Ig heavy chain pre  
1431 75.5 4.0 178 2 T20599 hypothetical prote  
1432 75.5 4.0 196 2 S50487 hypothetical prote  
1433 75.5 4.0 202 2 B87342 hypothetical prote  
1434 75.5 4.0 212 2 T10923 3C3.14c protein -  
1435 75.5 4.0 254 2 B31790 Ig heavy chain v r  
1436 75.5 4.0 261 2 C85681 hypothetical prote  
1437 75.5 4.0 280 1 B64235 fibronectin-bindin  
1438 75.5 4.0 290 2 I68750 MHC class I lympho  
1439 75.5 4.0 296 2 T94253 homeotic protein s  
1440 75.5 4.0 311 2 T04801 hypothetical prote  
1441 75.5 4.0 317 2 S55316 mucin (clone PGM-2  
1442 75.5 4.0 324 2 S55316 protein gp49 (Bact  
1443 75.5 4.0 341 2 C86307 F20D23.17 protein  
1444 75.5 4.0 346 1 D50474 hypothetical prote  
1445 75.5 4.0 346 1 D64811 adose 1-epimerase  
1446 75.5 4.0 353 2 G02922 MHC class I Lero-G  
1447 75.5 4.0 356 2 T31376 plant adhesion mol  
1448 75.5 4.0 357 2 S11141 class I histocoma  
1449 75.5 4.0 424 2 T33839 hypothetical prote  
1450 75.5 4.0 448 1 A29830 benzene 1,2-dioxvg  
1451 75.5 4.0 465 2 T29257 hypothetical prote  
1452 75.5 4.0 467 2 G59849 endo-1,4-beta-xyla  
1453 75.5 4.0 473 2 F70031 cell wall-binding  
1454 75.5 4.0 497 2 T51195 hypothetical prote  
1455 75.5 4.0 503 2 JC5287 SHP substrate-1 pr  
1456 75.5 4.0 510 2 H84824 En/spm-like transp  
1457 75.5 4.0 511 2 I50114 early growth respo  
1458 75.5 4.0 519 2 S23796 modifier-3 protein  
1459 75.5 4.0 519 2 A54590 GAGA transcription  
1460 75.5 4.0 531 2 S20900 titin - mouse (fira  
1461 75.5 4.0 593 2 JC7829 metal-responsive t  
1462 75.5 4.0 608 2 T37864 hypothetical prote  
1463 75.5 4.0 653 2 I48341 endoglin - mouse  
1464 75.5 4.0 671 2 A01666 DNA ligase homolog  
1465 75.5 4.0 699 2 I37369 epican - human  
1466 75.5 4.0 706 2 S53035 probable lysophosp  
1467 75.5 4.0 753 2 AE2009 cation-transportin  
1468 75.5 4.0 756 2 JC5886 signaling mediator  
1469 75.5 4.0 781 2 T51433 probable cation tr  
1470 75.5 4.0 816 2 S05548 gap protein hunchb  
1471 75.5 4.0 851 2 T38648 hypothetical prote  
1472 75.5 4.0 878 2 T21621 hypothetical prote  
1473 75.5 4.0 880 1 C41166 protein-tyrosine k  
1474 75.5 4.0 910 2 C69456 subtilisin sendai  
1475 75.5 4.0 929 2 I51027 type XII collagen  
1476 75.5 4.0 935 2 T19011 hypothetical prote  
1477 75.5 4.0 962 2 D86186 hypothetical prote  
1478 75.5 4.0 1013 2 T46422 hypothetical prote  
1479 75.5 4.0 1033 2 A12359 hypothetical prote  
1480 75.5 4.0 1064 2 B86465 probable Protein k  
1481 75.5 4.0 1093 2 I38533 AF17 protein - hum  
1482 75.5 4.0 1121 2 T38127 phosphoprotein pho  
1483 75.5 4.0 1171 2 A42916 metabotropic gluta  
1484 75.5 4.0 1240 2 T04833 hypothetical prote  
1485 75.5 4.0 1332 2 S41552 probable transcrip  
1486 75.5 4.0 1343 2 AF0611 cell division prot  
1487 75.5 4.0 1404 2 E85509 hypothetical prote  
1488 75.5 4.0 1404 2 E90658 Rnag core protein  
1489 75.5 4.0 1447 2 S02160 DNA topoisomerase

1490 75.5 4.0 1557 2 T18412 lipid-binding prot  
1491 75.5 4.0 1711 2 C71625 variant-specific s  
1492 75.5 4.0 1753 2 S30855 hypothetical prote  
1493 75.5 4.0 1807 2 JC6319 integrin beta-4 ch  
1494 75.5 4.0 2015 2 B81989 hypothetical prote  
1495 75.5 4.0 2610 2 T20968 hypothetical prote  
1496 75.5 4.0 2774 2 A43359 microtubule-associ  
1497 75.5 4.0 3869 2 A48205 Ali-1 protein +GTE  
1498 75.5 4.0 4377 2 A55575 ankyrin 3, long sp  
1499 75 3.9 107 2 D72598 hypothetical prote  
1500 75 3.9 138 2 A27639 T-cell receptor ga

## ALIGNMENTS

## RESULT 1

JC7780

coxackie- and adenovirus receptor - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 02-Apr-2002 #sequence\_revision 02-Apr-2002 #text\_change 09-Jul-2004

C;Accession: JC7780

R;Thoenen, I.; Keyaerts, E.; Lindberg, M.; Van Ranst, M.

Biochem. Biophys. Res. Commun. 288, 805-808, 2001

A;Title: Characterization of a cDNA encoding the bovine coxsackie and adenovirus receptor

A;Reference number: JC7780

A;Contents: Liver

A;Accession: JC7780

A;Molecule type: mRNA

A;Residues: 1-365 &lt;THO&gt;

A;Cross-references: UNIPROT:Q8WVU3; GB:AY033651

C;Comment: This protein serves as the primary adenoviral attachment site on bovine cells.

Query Match 24.8%; Score 474; DB 2; Length 365;

Best Local Similarity 33.6%; Pred. No. 1.1e-26;

Matches 128; Conservative 66; Mismatches 153; Indels 34; Gaps 11;

Qy 1 MSLLLLLL---VSYYVGTGTHTE---IKRVASEKVTLPCHQHLGPEKDTLDIEWLLT 54

Db 1 MELLRLFLLLCGVADFTRGSLITTPQOMIEKAGETAYLPCKFTLGPDPQGLDIEWLLS 60

Qy 55 --DNEGKQKVITYSSRHVNNLTERRQGRVAFASNEL-AGDASLIQIEPKPSDEGRYTC 111

Db 61 PADNQKQDVQIILSYSGDKIYDDYQDLKRGVHFTHSNDLKSGDGINVTNLQSLDGTGYQC 120

Qy 112 KVKNSGRYVWSHVLKVLVRSPKPKCELGSLTSGSLTLQCESSSGTEPIVYVQRIRE 171

Db 121 KVKAPGVGNKKIQITVLVFKPSGIRCYVDGSEETGNDFKLKCEPKESLPIRYEQKL-- 178

Qy 172 KEGEDERLPPKSRIDYNHPRVLLQNLTMYSGLYQCTAGNEAGKESCVRV-TVQYVQS 230

Db 179 --SDSKLPTSWLPMTSP-VISVKNASAEYSGTCTVRNRVGSQDCLLRDVLVPPSNR 235

Qy 231 IGWAGAVTGIVAGALLIFLLVLLIRKDKERYEEERPNREIDAEAPKARLVKPPSS 290

Db 236 AGTTAGAVTGITLLALVLIALIVFCCHKREKEKEVH-HDIREDDVPPKSRSTARSY 294

Qy 291 SSGSRSSRSGSSSTRSTANSASRSORTLSTD--AAPO-PGLATQAYSLVGPEVRGSEPKK 347

Db 295 IGSNHSILGSMSPNMEGYKTYNQVPSDELRAPOSPTL-----PPAK 339

Qy 348 VHAHLTKAETTPSMIFPSQS 368

Db 340 VAAPNLSRMGAVPVWIPQAQSK 360

## RESULT 2

S56749

junctional adhesion molecule precursor - human

N;Alternate names: F11 platelet antigen; platelet adhesion molecule PAM-1; platelet F11

C;Species: Homo sapiens (man)

C;Date: 27-Oct-1995 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004

C;Accession: A59406; S56749



Db 115 TQHEPKTSQVYLIVQVPPKISNISSDVTVNEGNTVLCMANGREPVI-TWRHLTPGTR 173  
Qy 171 EKEGEDERLPPKSRIDYNHNGRVLQNLTMYSGLYQCTAGNEAKGESC-VVRVTQVQVQ 229  
Db 174 EPEGEEVLE-----ILGITREQSGKYCKAANEVSSADVKQVKVTNVP 219  
Qy 230 SI-CMVAGAVTG-----IVAGALLIFLLWLLTRDKKERYEERPNREIDAEAPK 281  
Db 220 TITESKSNEATTGROASKCEASA-----VPAPDFEYRDDTRIN----- 259  
Qy 282 ARLVKPSSSSSGSRSSGSTRSTANSASRSQRTSLTDAAPQGLATQAYSLVGP-EV 340  
Db 260 -----SANGLEIKSTEGQSSLLTVNTEHYGNYTCVAANKLCVNTASLVLPQSV 311  
Qy 341 RG 342  
Db 312 RG 313

RESULT 5  
RWHC2  
T-cell surface glycoprotein CD2 precursor - human  
N:Alternate names: E rosette receptor; erythrocyte receptor; erythrocyte-binding protein  
C:Species: Homo sapiens (man)  
C:Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 09-Jul-2004  
C:Accession: A28967; A26486; B26486; A28416; A28023; S02292; A30430; S00829; A29874  
R:Diamond, D.J.; Clayton, L.K.; Sayre, P.H.; Reinherz, E.L.  
Proc. Natl. Acad. Sci. U.S.A. 85, 1615-1619, 1988  
A:Title: Exon-intron organization and sequence comparison of human and murine T11 (CD2)  
A:Reference number: A28967; MUID: 88144486; PMID: 2894031  
A:Accession: A28967  
A:Molecule type: DNA  
A:Residues: 1-351 <DIA>  
A:Cross-references: UNIPROT:P06729; GB:M19806; GB:J03622; GB:J03623; NID:g180079; PIDN:A  
R:Sewell, W.A.; Brown, M.H.; Dunne, J.; Owen, M.J.; Crumpton, M.J.  
Proc. Natl. Acad. Sci. U.S.A. 83, 8718-8722, 1986  
A:Title: Molecular cloning of the human T-lymphocyte surface CD2 (T11) antigen.  
A:Reference number: A26486; MUID: 87041523; PMID: 3490670  
A:Accession: A26486  
A:Molecule type: mRNA  
A:Residues: 1-338, 'M', 340, 'QKTHCPLPLIKDRNCLFQ' <SE1>  
A:Accession: B26486  
A:Molecule type: protein  
A:Residues: 25-46, 'X', 50 <SE2>  
R:Sewell, W.A.; Brown, M.H.; Dunne, J.; Owen, M.J.; Crumpton, M.J.  
Proc. Natl. Acad. Sci. U.S.A. 84, 7256, 1987  
A:Reference number: A28416  
A:Contents: revision  
A:Accession: A28416  
A:Molecule type: mRNA  
A:Residues: 333-351 <SE3>  
R:Seed, B.; Aruffo, A.  
Proc. Natl. Acad. Sci. U.S.A. 84, 3365-3369, 1987  
A:Title: Molecular cloning of the CD2 antigen, the T-cell erythrocyte receptor, by a rap  
A:Reference number: A28023; MUID: 87204137; PMID: 2437578  
A:Accession: A28023  
A:Molecule type: mRNA  
A:Residues: 1-265, 'Q', 267-351 <SEE>  
A:Cross-references: GB:M16445; NID:g178668; PIDN:AAA51738.1; PID:g178669  
R:Sayre, P.H.; Chang, H.C.; Hussey, R.E.; Brown, N.R.; Richardson, N.E.; Spagnoli, G.; C  
Proc. Natl. Acad. Sci. U.S.A. 84, 2941-2945, 1987  
A:Title: Molecular cloning and expression of T11 cDNAs reveal a receptor-like structure  
A:Reference number: S02292; MUID: 87204243; PMID: 2883656  
A:Accession: S02292  
A:Molecule type: mRNA  
A:Residues: 1-338, 'M', 340, 'QKTHCPLPLIKDRNCLFQ' <SA1>  
A:Cross-references: GB:M16336; NID:g180093; PIDN:AAA51946.1; PID:g180094  
A:Accession: A30430  
A:Molecule type: protein  
A:Residues: 25-43, 152-163 <SA2>  
R:Liang, G.; Wootton, D.; Owen, M.J.; Sewell, W.A.; Brown, M.H.; Mason, D.Y.; Crumpton, M.  
EMBO J. 7, 1675-1682, 1988  
A:Title: The structure of the human CD2 gene and its expression in transgenic mice.

A:Reference number: S00829; MUID: 89005055; PMID: 2901953  
A:Accession: S00829  
A:Molecule type: DNA  
A:Residues: 1-351 <LAN>  
A:Cross-references: EMBL:X07871  
C:Comment: CD2 is a surface antigen expressed on all peripheral blood T-cells. It appears  
or is closely associated with, the erythrocyte receptor.  
C:Genetics:  
A:Gene: GDB:CD2  
A:Cross-references: GDB:118735; OMIM:186990  
A:Map position: 1p13.1-1p13.1  
A:Introns: 21/1; 128/1; 205/1; 246/1  
C:Superfamily: T-cell surface glycoprotein CD2  
C:Keywords: glycoprotein; T-cell; transmembrane protein  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-351/Product: T-cell surface glycoprotein CD2 #status predicted <MAT>  
F:25-206/Domain: extracellular #status predicted <EXT>  
F:210-234/Domain: transmembrane #status predicted <TM>  
F:237-351/Domain: intracellular #status predicted <INT>  
F:89,141,150/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.5%; Score 182; DB 1; Length 351;  
Best Local Similarity 25.1%; Pred. No. 1.1e-05;  
Matches 89; Conservative 51; Mismatches 128; Indels 86; Gaps 17;

Qy 45 DTLDEIWLTLTNEG----QKVTYSSRHVYNNLTTEQKGRVAPASNPLAGDASLQIEP 100  
Db 53 DDDIKWEKTSKKKIAQFRKEKTEKDYK-----LFKNGTLKIKH 96  
Qy 101 LKPSDEGRYTCVKNS-GRYVSHVI-LKLVRSKPK----CELEGELTSGDLTLOCE 154  
Db 97 LKDDQDIYKVSIIYDTGKNVLEKIFDLKIQERVSKPKISWTC-----INTLTCE 147  
Qy 155 SSSGTETIVYVQRIREKEGEDERLPPKSRIDYNHNGRVLQNLTMYSGLYQCTAGNEA 214  
Db 148 VMNGTDELNLYQ-----DGKHLKLSQ-----RVITHKWTLSAKFKCTAGNKV 192  
Qy 215 GKESCVRVTQVYQSIGMVAGAVTGIVAGALLIPLLVLLI-----RRKKERYEEBER 269  
Db 193 SKSSSEVPVS---CPEKGLDIYLIIGICGGSLLMVALLVFFYITKTKKQSRRENDEL 249  
Qy 270 PNEIREDAEAPKALVKPSSSSSGSRSSSTRSTANSASRSQRTSLTDAAPQPG-- 327  
Db 250 --ETRAHRVATEERGRKPHQIPAS--TPQNPAATSQHPPPPPGHRSQ--APSHRPPPPGHR 303  
Qy 328 -----LATQAYSLVGPEVRGS--BPKKVHHANLTKAETTPSMIFSQS 367  
Db 304 VHQPKPKPPAPSGTQVHQKGPPLPRPVQPKPHGA----AEN--SLSPSSN 351

## RESULT 6

T20992  
hypothetical protein F15G9.4a - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T20992; T24733  
R:Sulston, J.  
submitted to the EMBL Data Library, December 1994  
A:Reference number: Z19355  
A:Accession: T20992  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-5175 <WIL>  
A:Cross-references: UNIPROT:Q810L3; EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN00028; CESP:F15  
R:Kershaw, J.  
submitted to the EMBL Data Library, December 1994  
A:Reference number: Z19929  
A:Accession: T24733  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-5175 <W12>  
A:Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:F15G9.4a

A;Experimental source: clone T09B9

C;Genetics:

A;Gene: CESP:F15G9.4a

A;Map position: X

A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3; 1251/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1; 3033/1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5077/1

Query Match 9.3%; Score 178; DB 2; Length 5175;

Best Local Similarity 26.0%; Pred. No. 0.0006;

Matches 54; Conservative 31; Mismatches 81; Indels 42; Gaps 7;

Qy 21 TEIKRVAEEKVTLPCCHQHLGPEKDTLDIEWLLTDNEGKQKVITYSSRRHVNINLTERQK 80

Db 3045 TEI--VADTTLEIPRTE-GIPPP--EISWFLDGKPILEMPGVYKQ----- 3086

Qy 81 GRVAFASNFLAGDASLOIEPLKPSDEGRYTCVKNSGRYVSHVILKVLVLRPSKPCBLE 140

Db 3087 -----GDLRLIDNIKPNQEGRYTCAENKAGRAEQDTYVEISEPVRVMASEV 3135

Qy 141 GELTEGSDLTQCESSSGTEPIVYVQRIREKEGE---DERLPPKSRIDYVNHGPRVLLQN 197

Db 3136 MRVVEGRQTTIRCEVFGNPEPVNWL-----KDGEPYTSLLQFSTKLSYLH-----LRE 3185

Qy 198 LTMSYGLYQCTAGNEAGKESCVVRVTV 225

Db 3186 TTLADGGTYTCTIATNKAGESQTTTDEVEV 3213

RESULT 7

T43290

hemocentin precursor - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 11-Jan-2000 #sequence revision 11-Jan-2000 #text\_change 09-Jul-2004

C;Accession: T43290; T20993; T24734

R;Vogel, B.E.; Hedgecock, E.M.

A;Description: Hemocentin is required for hemidesmosome mediated cell adhesion and germ-

A;Reference number: Z23396

A;Accession: T43290

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-5198 <VOG>

A;Cross-references: UNIPROT:O76518; EMBL:AF074901; PIDN:AAC26792.1

R;Sulston, J.

A;Reference number: Z19355

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Accession: T20993

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-5198 <WIL>

A;Cross-references: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN000028; CESP:F15G9.4b

A;Experimental source: clone F15G9

R;Kershaw, J.

A;Reference number: Z19929

A;Accession: T24734

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-5198 <W12>

A;Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN000028; CESP:F15G9.4b

A;Experimental source: clone T09B9

C;Genetics:

A;Gene: him-4; F15G9.4b

A;Map position: X

A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;

2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1;

1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/

Query Match 9.3%; Score 178; DB 2; Length 5198;

Best Local Similarity 26.0%; Pred. No. 0.00061;

Matches 54; Conservative 31; Mismatches 81; Indels 42; Gaps 7;

Qy 21 TEIKRVAEEKVTLPCCHQHLGPEKDTLDIEWLLTDNEGKQKVITYSSRRHVNINLTERQK 80

Db 3045 TEI--VADTTLEIPRTE-GIPPP--EISWFLDGKPILEMPGVYKQ----- 3086

Qy 81 GRVAFASNFLAGDASLOIEPLKPSDEGRYTCVKNSGRYVSHVILKVLVLRPSKPCBLE 140

Db 3087 -----GDLRLIDNIKPNQEGRYTCAENKAGRAEQDTYVEISEPVRVMASEV 3135

Qy 141 GELTEGSDLTQCESSSGTEPIVYVQRIREKEGE---DERLPPKSRIDYVNHGPRVLLQN 197

Db 3136 MRVVEGRQTTIRCEVFGNPEPVNWL-----KDGEPYTSLLQFSTKLSYLH-----LRE 3185

Qy 198 LTMSYGLYQCTAGNEAGKESCVVRVTV 225

Db 3186 TTLADGGTYTCTIATNKAGESQTTTDEVEV 3213

RESULT 8

PN0568

connectin 3B - chicken (fragment)

N;Alternate names: Cn3B protein

C;Species: Gallus gallus (chicken)

C;Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 09-Jul-2004

C;Accession: PN0568

R;Maruyama, K.; Endo, T.; Kume, H.; Kawamura, Y.; Kanzawa, N.; Nakachi, Y.; Kimura, S.;

Biochem. Biophys. Res. Commun. 194, 1288-1291, 1993

A;Title: A novel domain sequence of connectin localized at the 1 band of skeletal muscle

A;Reference number: PN0568; MUID:9335802; PMID:8352787

A;Accession: PN0568

A;Residues: 1-1323 <MAR>

A;Cross-references: UNIPROT:Q08476; DDBJ:D16541; NID:G391629; PID:d1004495; PID:G391630

A;Experimental source: skeletal muscle

C;Comment: This protein string-like single molecule spans from the Z line to the M line ;

Query Match 8.6%; Score 163.5; DB 2; Length 1323;

Best Local Similarity 27.3%; Pred. No. 0.0012;

Matches 75; Conservative 34; Mismatches 107; Indels 59; Gaps 15;

Qy 10 VSYVVTGLTGTTEIKRV-----AEEKVTLPCHQHLGPEKD-----TLIDEWL 52

Db 420 ISYVENT--AHLTILRVDRGDSGRYTCYASNEVGKDSCTAQLNKKERTPTPTTRKUSEA 477

Qy 53 LTDNEGN-----QKVIVTVSSRRHVNINLTERQK--RVAFASNFLAGDASLOI 98

Db 478 VEETEGNELKLEGRVAGSQPLTVSW-----YNNQEVHSSPHCEISFKNTLL-----LHI 528

Qy 99 EPLKPSDEGRYTCVKNSGRYV--WSHVILKVLVLRPSKPC---ELEGELT-EGSDLTQ 152

Db 529 KSVGSDAGLYTCVKNSAGSVLCTSSVIV--EPKPPVPDQPLQPAATEEGDTLQLS 585

Qy 153 CESSSGTEPIVYVQRIREKEGEDERLPPKSRIDY-NHGPGRVLLONLTMSVGLYQCTAG 211

Db 586 CH-VRGSEPIRIQWL---KAGREIRASERCSFSGFANGVALLEAAVTKSDSGEYVCKAS 640

Qy 212 NEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGAL 246

Db 641 NVAGTDCRSKVTVK--EKAALVSAAKKADIEGKL 673

RESULT 9

S03199

opioid-binding protein OPCAM precursor - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 09-Jul-2004

C;Accession: S03199

R;Schofield, P.R.; McFarland, K.C.; Hayflick, J.S.; Wilcox, J.N.; Cho, T.M.; Roy, S.; Lee

EMBO J. 8, 489-495, 1989

A;Title: Molecular characterization of a new immunoglobulin superfamily protein with pote

A;Reference number: S03199; MUID:89251576; PMID:2721489

A;Accession: S03199

A;Molecule type: mRNA

A;Residues: 1-345 <SCH>





A;Accession: T42633  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-4162 <YAJ>  
A;Cross-references: UNIPROT:Q98918; EMBL:D83390; NID:g1513029; PIDN:BAAL1908.1; PID:g1513029  
A;Experimental source: breast muscle  
C;Keywords: skeletal muscle

Query Match 8.3%; Score 159; DB 2; Length 4162;  
Best Local Similarity 26.9%; Pred. No. 0.011;  
Matches 60; Conservative 38; Mismatches 97; Indels 28; Gaps 10;

Qy 58 GNQKVITYSSRRHVNNLTETQKGRVAFASFLAGDASLQIEPLKPSDEGRYTCVKVNSG 117  
Db 3302 GSPEIKVTV-----YKGETEHPSE-KYSMFVDSVAVLEMHNLVSDESGYSCAQNPA 3355  
Qy 118 RYVMSHVILKVLVRPSKPCBLEGTSGDLTLQCESSSGTEPIVYVQRIREKEGSE 177  
Db 3356 GSASTSTSLKVKAPAFATKKPHPVQTLKGSVDHLECE-LQGTTPPQISWY---KDKREI 3410  
Qy 178 RLPPKSRI-DYNHPRVLLQNLWTSYGLYQCTAGNEAGKSCVVRVT-----VQTVQ 229  
Db 3411 RSSKKYKVMSENYLASIHILNVDADVGHYHCKAVNDVGSDCIGSVTLRAPPTFVKKLS 3470  
Qy 230 SIGWAG---AVTGIVAGALLIFLLVLLIRRKOK-ERYEERE 268  
Db 3471 DTVVVVGETIELQAAVEGAQPISVL-WL-----KDKGEIIRSE 3508

RESULT 13  
JC4025  
opioid-binding cell adhesion protein - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jun-1995 #sequence\_revision 14-Jul-1995 #text\_change 09-Jul-2004  
C;Accession: JC4025  
R;Shark, K.B.; Lee, N.M.  
Gene 155, 213-317, 1995  
A;Title: Cloning, sequencing and localization to chromosome 11 of a cDNA encoding a human  
A;Reference number: JC4025; MUID:95237612; PMID:7721093  
A;Accession: JC4025  
A;Molecule type: mRNA  
A;Residues: 1-345 <SHA>  
A;Cross-references: UNIPROT:Q14982; GB:L34774; NID:g514373; PIDN:AAA36387.1; PID:g514374  
A;Experimental source: brain  
C;Comment: This protein binds opioid alkaloids in the presence of acidic lipids, exhibits  
C;Genetics:  
A;Gene: GDB:OPCWL; OBCAM; OPCM  
A;Cross-references: GDB:251677; OMIM:600632  
A;Map position: 11pter-11qter  
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin

Query Match 8.3%; Score 158; DB 2; Length 345;  
Best Local Similarity 23.0%; Pred. No. 0.00057;  
Matches 76; Conservative 39; Mismatches 129; Indels 86; Gaps 11;

Qy 29 EKVTLPCHHQLGLPEKDILD-----IEWLLTDN-----EGNQK-----VVITYSSRRHVNN 74  
Db 51 ESATLRC-----TIDRVRTVAMLRNRSTILYAGNDKWSIDPRVILVNTPTQY-- 98  
Qy 75 LTEEQKRVAFASFLAGDASLQIEPLKPSDEGRYTCVKVNSGRYVMSHVILKVLVRPSK 134  
Db 99 -----SIMIQNVDVDEGPTCSVQTDNHPKTSRVHLIVQVPQI 138  
Qy 135 PKCELEGELTEGSDTLQCESSSGTEPIVYVQRIREKEG-----EDRLPPKSRIDVNH 189  
Db 139 MNISDITVNEGSSVTLLCLAIGREPTV-TWRHLSVKEGQGQGVSEDEYLE----- 188  
Qy 190 PGRVLLQNLWTSYGLYQCTAGNE-AGKESCVRVTYVQVQSIGMVAGAVTIVAGALLI 248  
Db 189 -----ISDIKRQDSGEYECSSALNDVAAPDVRKVKITVNPYPYISKAKN--TCVSVGQKGI 241  
Qy 249 FLVLLVLLIRRKDKERYEEREENREIDAEAPKARLVKPPSSSSSGSRSSRSGSSSTRSTA 308

Db 242 LSCBASAVPMAEFQWFKEETR-----LATLQDMRIENKGRMSTLTFF 284  
Qy 309 NSASRSQRTLTSDAAPQPLATQAYSVLGP 338  
Db 285 NVSEKDYGNVTCVATNKLGNATNATITLYGP 314

RESULT 14  
I38346  
elastic titin - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
C;Accession: I38346  
R;Labeit, S.; Kolmerer, B.  
Science 270, 293-296, 1995  
A;Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.  
A;Reference number: A57430; MUID:96026330; PMID:7569978  
A;Accession: I38346  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-7962 <RES>  
A;Cross-references: UNIPROT:Q10465; EMBL:X90569; NID:g1017426; PIDN:CAA62189.1; PID:g1017426  
C;Genetics:  
A;Gene: GDB:TTN  
A;Cross-references: GDB:I27867; OMIM:188840  
A;Map position: 2q31-2q31

Query Match 8.3%; Score 158; DB 2; Length 7962;  
Best Local Similarity 22.3%; Pred. No. 0.028;  
Matches 86; Conservative 60; Mismatches 166; Indels 74; Gaps 16;

Qy 35 CHHQLGLPEK---DTLDIEWLLTDNE-----GNQKVITYSSRRHVNNLTETEOKG 81  
Db 3960 CSAQLGVQEPFRFTKKLEPSRIVKQDEFTRYECKIGSGPEIKVLW-----YKDETEIQES 4014  
Qy 82 RVAFASFLAGDASLQIEPLKPSDEGRYTCVKVNSGRYVMSHVILKVLVRPSKPKCELEG 141  
Db 4015 S-KFRMSFVDSVAVLEMHNLVSDESGDYTCFAHNAAGSASSSTLSKVKEPPIFRKKPHPI 4073  
Qy 142 ELTEGSDTLQCESSSGTEPIVYVQRIREKEGEDERLPKPSRI-DYNHPRVLLQNLTM 200  
Db 4074 ETLKGAADVHLECE-LQGTTPPFHVSWY-----KDKRELRSKKYKIMSENFLTSTHILNLYDA 4128  
Qy 201 SYSGLYQCTAGNEAGKSCVVRVT-----VQVQSIGMVAGAVTGI---VAGALLIFL 250  
Db 4129 ADIGEYQCKATNDVGSDDTCVGSIALKAPPRFVKLSLSDISTVVGKEVQIOTTIEGAEP1-S 4187  
Qy 251 LVWL-----LIRRKDK-----ERYEERPN-----EIREDAEAPKA-----RL 284  
Db 4188 VVWFKDKGEIVRESDNIIWISYSENIATLQFSRVBPANAGKVTQIKNDAGMQECFATLSV 4247  
Qy 285 VKPSSSSSGSRSSSGSSSTRSTANSASRSORTLSTDAAPQPLATQAYSVLGPVEVRS 344  
Db 4248 LEPATIVEKPSISKVTGDT-----CTLECTVAGTPELSTKWFK-DGKELTSDN 4295

Qy 345 PKVHHANLTAEITTPSMIPQSRAF 370  
Db 4296 KYKISFFNKVSGLKIINVAPSDSGVI 4321

RESULT 15  
A37821  
butyrophilin - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 30-Apr-1991 #sequence\_revision 30-Apr-1991 #text\_change 09-Jul-2004  
C;Accession: A37821  
R;Jack, L.J.W.; Mather, I.H.  
J. Biol. Chem. 265, 14481-14486, 1990  
A;Title: Cloning and analysis of cDNA encoding bovine butyrophilin, an apical glycoprotein  
A;Reference number: A37821; MUID:90354441; PMID:2387867  
A;Accession: A37821  
A;Status: preliminary





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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: May 5, 2005, 08:01:29 ; Search time 171 Seconds  
(without alignments)  
1116.991 Million cell updates/sec

Title: US-09-978-375A-59

Perfect score: 1908

Sequence: 1 NSLLLLLLLVYVGTGLGTH.....TKAETTPSNIPQSRAFQTV 373

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	1908	100.0	373	2	QH6B4	Q9h6b4	homo sapien
2	1781	93.3	372	2	Q8K1G0	Q8k1g0	rattus norv
3	1763.5	92.4	373	2	Q8R373	Q8r373	mus musculus
4	1759.5	92.2	373	2	Q920S5	Q920s5	mus musculus
5	787.5	41.3	332	2	Q640U3	Q640u3	xenopus tro
6	592.5	31.1	160	2	Q6C1H8	Q6c1h8	mus musculus
7	487.5	25.6	372	2	Q90Y50	Q90y50	brachydanio
8	474	24.8	365	2	Q8WMV3	Q8wmv3	bos taurus
9	465	24.4	365	1	CXAR_HUMAN	P78310	homo sapien
10	463	24.3	358	2	Q9R066	Q9r066	rattus norv
11	457.5	24.0	365	1	CXAR_MOUSE	P97792	mus musculus
12	457.5	24.0	365	2	Q9DBJ8	Q9dbj8	mus musculus
13	443	23.2	319	2	Q9TU79	Q9tu79	sus scrofa
14	434.5	22.8	344	2	Q9UKV4	Q9ukv4	homo sapien
15	433.5	22.7	344	2	Q9R067	Q9r067	rattus norv
16	433	22.7	319	2	Q9TU80	Q9tu80	canis famil
17	422.5	22.1	352	2	Q91W66	Q91w66	mus musculus
18	407.5	21.4	298	2	Q804R4	Q804r4	brachydanio
19	362.5	19.0	430	2	Q8N4F1	Q8n4f1	homo sapien
20	336	17.6	237	2	Q6DQX5	Q6dqx5	ryctolagus
21	335	17.6	394	2	Q6AYD4	Q6ayd4	rattus norv
22	321.5	16.9	390	2	Q95K13	Q95k13	macaca fasc
23	321	16.8	394	2	Q925F2	Q925f2	mus musculus
24	320.5	16.8	323	2	Q8NDD2	Q8ndd2	homo sapien
25	317.5	16.6	407	2	Q9D2J4	Q9d2j4	mus musculus
26	314.5	16.5	325	2	Q95791	Q95791	homo sapien
27	309.5	16.2	327	2	Q961O7	Q961o7	homo sapien
28	308.5	16.2	319	1	A33_HUMAN		
29	307.5	16.1	390	2	Q96AP7	Q96ap7	homo sapien
30	305.5	16.0	390	2	Q96T50	Q96t50	homo sapien
31	300.5	15.7	304	2	Q9CVA4	Q9cva4	mus musculus

32	299.5	15.7	248	2	Q9D0T4	Q9d0t4	mus musculus
33	296.5	15.5	406	2	Q8N7T8	Q8n7t8	homo sapien
34	295	15.5	387	2	Q86XK7	Q86xk7	homo sapien
35	295	15.5	412	2	Q6MZS4	Q6mzs4	homo sapien
36	283	14.8	335	2	Q9PWR4	Q9pwr4	gallus gall
37	282	14.8	284	2	Q9NX42	Q9nx42	homo sapien
38	280.5	14.7	259	2	Q7Z2Q1	Q7z2q1	homo sapien
39	278.5	14.6	252	2	Q8WWT6	Q8wwt6	homo sapien
40	278.5	14.6	319	1	A33_MOUSE		
41	277	14.5	335	2	Q9YGH1	Q9ygh1	gallus gall
42	275.5	14.4	335	2	Q9YGV5	Q9ygv5	gallus gall
43	273.5	14.3	328	2	Q9Z1O9	Q9z1o9	mus musculus
44	269.5	14.1	300	2	Q9D9U0	Q9d9u0	mus musculus
45	267	14.0	318	2	Q91664	Q91664	xenopus lae
46	266.5	14.0	300	2	Q9DA22	Q9da22	mus musculus
47	265	13.9	432	2	Q6DDE7	Q6dde7	xenopus lae
48	263.5	13.8	442	2	Q6NWB8	Q6nwb8	brachydanio
49	261.5	13.7	332	2	Q6P359	Q6p359	xenopus tro
50	256	13.4	305	2	Q6P3A4	Q6p3a4	mus musculus
51	214.5	11.2	390	2	Q6P500	Q6p500	rattus norv
52	205.5	10.8	292	2	Q66I72	Q66i72	brachydanio
53	200.5	10.5	300	2	Q9JHY1	Q9jhy1	rattus norv
54	196	10.3	299	1	JAM1_HUMAN		
55	195.5	10.2	300	2	Q8VC39	Q8vc39	homo sapien
56	193.5	10.1	298	1	JAM1_BOVIN		
57	193.5	10.1	309	2	Q96FL1	Q96fl1	homo sapien
58	193.5	10.1	310	1	JAM3_HUMAN		
59	193	10.1	181	2	Q91665	Q91665	xenopus lae
60	190	10.0	300	1	JAM1_MOUSE		
61	189.5	9.9	338	1	LAMP_CHICK		
62	188	9.9	280	2	Q737I6		
63	188	9.9	338	1	LAMP_RAT		
64	187	9.8	338	1	LAMP_HUMAN		
65	186	9.7	350	2	O028F9	O028f9	gallus gall
66	185	9.7	200	2	Q8WWT7	Q8wwt7	homo sapien
67	185	9.7	334	2	O02870	O02870	gallus gall
68	185	9.7	337	2	Q6GLZ7	Q6glz7	xenopus lae
69	184.5	9.7	341	1	LAMP_MOUSE		
70	184	9.6	164	2	Q99KG0	Q99kg0	mus musculus
71	183	9.6	351	1	CD2_HUMAN		
72	181	9.5	345	2	Q6SZ63	Q6sz63	pan troglod
73	181	9.5	510	2	Q96K15	Q96k15	homo sapien
74	180.5	9.5	289	2	Q7ZWT0	Q7zwt0	xenopus lae
75	180.5	9.5	344	2	Q6SZ62	Q6sz62	papio anubi
76	180	9.4	350	2	Q6SZ59	Q6sz59	cercocebus
77	178	9.3	508	2	Q8CED8	Q8ced8	mus musculus
78	178	9.3	508	2	Q8R007	Q8r007	mus musculus
79	178	9.3	5175	2	Q810L3	Q810l3	caenorhabdi
80	178	9.3	5198	2	Q76518	Q76518	caenorhabdi
81	177.5	9.3	334	2	Q6SZ56	Q6sz56	macaca nene
82	177.5	9.3	341	2	Q6SZ57	Q6sz57	macaca arct
83	176.5	9.3	351	2	Q6SZ61	Q6sz61	macaca fasc
84	175.5	9.2	484	2	Q26475	Q26475	schistocerc
85	175	9.2	340	2	Q764N3	Q764n3	sus scrofa
86	174.5	9.1	345	2	Q6SZ58	Q6sz58	macaca assa
87	174	9.1	483	2	Q9DBP8	Q9dbp8	mus musculus
88	173	9.1	510	2	Q96NY8	Q96ny8	homo sapien
89	171.5	9.0	298	2	Q8C5K9	Q8c5k9	mus musculus
90	171	9.0	3410	2	Q7TN00	Q7tn00	rattus norv
91	169.5	8.9	585	2	Q6UY09	Q6uy09	homo sapien
92	169	8.9	413	2	Q7QBV2	Q7qbv2	anopheles g
93	168.5	8.8	351	2	Q6SZ60	Q6sz60	macaca mula
94	167.5	8.8	291	2	Q66J15	Q66j15	xenopus tro
95	167.5	8.8	298	1	JAM2_HUMAN		
96	167.5	8.8	310	2	Q86FQ2	Q86fq2	rattus norv
97	166	8.7	495	2	Q9HCY1	Q9hcy1	homo sapien
98	165.5	8.7	298	2	Q9J159	Q9j159	m vascular
99	164.5	8.6	662	2	Q60926	Q60926	homo sapien
100	164	8.6	438	2	Q920C3	Q920c3	mus musculus
101	164	8.6	509	2	Q920C2	Q920c2	mus musculus
102	164	8.6	529	2	Q91V87	Q91v87	mus musculus
103	163.5	8.6	298	2	Q6YNC1	Q6ync1	homo sapien
104	163.5	8.6	312	2	Q6UXG6	Q6uxg6	homo sapien

105	163.5	8.6	1323	2	Q08476	Q08476 gallus gall	178	150	7.9	765	2	Q9BKQ1	Q9bkq1 aplysia cal
106	163	8.5	3950	2	Q7YRF5	Q7yrf5 canis famil	179	150	7.9	812	2	Q9BKQ0	Q9bkq0 aplysia cal
107	162.5	8.5	298	2	Q8CE95	Q8ce95 mus musculu	180	149.5	7.8	545	2	Q9VCT4	Q9vct4 drosophila
108	162	8.5	584	2	Q00478	Q00478 homo sapien	181	149.5	7.8	727	1	PECL_MOUSE	Q0481 mus musculu
109	161.5	8.5	310	2	Q9D1M9	Q9d1m9 mus musculu	182	149.5	7.8	808	1	FGR4_MOUSE	Q03142 mus musculu
110	161.5	8.5	310	2	Q9D8B7	Q9d8b7 mus musculu	183	149.5	7.8	1235	2	Q86BD5	Q86bd5 drosophila
111	161.5	8.5	310	2	Q9EPK4	Q9epk4 m junctiona	184	149.5	7.8	1235	2	Q9V787	Q9v787 drosophila
112	161	8.4	577	2	Q80Y42	Q80y42 mus musculu	185	148.5	7.8	286	2	Q46535	Q46535 bos taurus
113	161	8.4	577	2	Q9D221	Q9d221 m mus muscu	186	148.5	7.8	344	1	CD2_RAT	Q08921 rattus norv
114	160.5	8.4	1431	2	Q80U60	Q80u60 mus musculu	187	148.5	7.8	533	2	Q8NCB6	Q8ncb6 homo sapien
115	160	8.4	345	1	OPCM_BOVIN	P11834 bos taurus	188	148.5	7.8	535	2	Q6UXG8	Q6uxg8 homo sapien
116	159.5	8.4	347	1	CD2_HORSE	P37998 equus caball	189	148.5	7.8	738	1	PECL_HUMAN	P16284 homo sapien
117	159	8.3	438	2	Q9JL87	Q9jlb7 mus musculu	189	148.5	7.8	799	2	Q8C3V5	Q8c3v5 mus musculu
118	159	8.3	510	2	Q9JL88	Q9jlb8 mus musculu	190	148.5	7.8	799	2	Q8CIB8	Q8cib8 mus musculu
119	159	8.3	713	2	Q90330	Q90330 coturnix co	191	148.5	7.8	799	2	Q6WRI0	Q6wri0 homo sapien
120	159	8.3	4162	2	Q98918	Q98918 gallus gall	192	148.5	7.8	2623	2	Q6WRI0	Q6wri0 homo sapien
121	158.5	8.3	296	2	Q640C0	Q640c0 xenopus lae	193	148.5	7.8	3707	1	PEGM_MOUSE	Q05793 mus musculu
122	158.5	8.3	300	2	Q7SYQ7	Q7syq7 xenopus lae	194	148	7.8	344	2	Q8N225	Q8n225 homo sapien
123	158.5	8.3	399	2	Q9Y279	Q9y279 homo sapien	195	148	7.8	344	2	Q93242	Q93242 gallus gall
124	158.5	8.3	1496	2	Q92626	Q92626 homo sapien	196	148	7.8	363	3	Q6NV41	Q6nv41 brachydanio
125	158	8.3	338	2	Q7Z3W6	Q7z3w6 homo sapien	197	148	7.8	847	1	CD22_HUMAN	P20273 homo sapien
126	158	8.3	345	1	OPCM_HUMAN	Q14982 homo sapien	198	148	7.8	5636	2	Q6BRW7	Q6brw7 homo sapien
127	158	8.3	394	2	Q86YT9	Q86yt9 homo sapien	199	147.5	7.7	344	2	Q6B014	Q6b014 homo sapien
128	158	8.3	7962	2	Q10465	Q10465 homo sapien	200	147.5	7.7	344	2	Q6P660	Q6p660 homo sapien
129	157	8.2	639	2	Q96P30	Q96p30 homo sapien	201	147.5	7.7	353	1	CEPU_CHICK	Q57596 gallus gall
130	157	8.2	734	2	Q96LA4	Q96la4 homo sapien	202	147	7.7	315	2	Q9DGI5	Q9dgi5 gallus gall
131	157	8.2	734	2	Q96P31	Q96p31 homo sapien	203	147	7.7	315	2	Q9DGI5	Q9dgi5 gallus gall
132	157	8.2	740	2	Q96P29	Q96p29 homo sapien	204	147	7.7	348	1	NEGR_MOUSE	Q08224 mus musculu
133	157	8.2	742	2	Q8N6S2	Q8n6s2 homo sapien	205	147	7.7	2013	2	Q7ZXX1	Q7zxx1 xenopus lae
134	157	8.2	807	2	Q6NY23	Q6ny23 brachydanio	206	147	7.7	765	2	Q9TWA4	Q9twa4 aplysia cal
135	156.5	8.2	544	2	Q6UX18	Q6ux18 homo sapien	207	147	7.7	812	2	Q9TWA5	Q9twa5 aplysia cal
136	156	8.2	344	1	NTRI_MOUSE	Q99pj0 mus musculu	208	147	7.7	932	2	Q9BKP9	Q9bkp9 aplysia cal
137	156	8.2	344	1	NTRI_RAT	Q92718 rattus norv	209	147	7.7	932	2	Q9TWA6	Q9twa6 aplysia cal
138	156	8.2	344	2	Q8BG33	Q8bg33 m mus muscu	210	147	7.7	1598	2	Q8P214	Q8p214 homo sapien
139	156	8.2	697	2	Q8NC72	Q8nc72 homo sapien	211	147	7.7	2013	2	Q9VHZ8	Q9vzh8 rattus norv
140	156	8.2	1059	2	Q6UXL7	Q6uxl7 homo sapien	212	147	7.7	404	1	RAGE_HUMAN	Q9erc8 mus musculu
141	156	8.2	1119	2	Q6UXM1	Q6uxm1 homo sapien	213	146.5	7.7	484	2	Q6BE00	Q6be00 xenopus lae
142	156	8.2	34350	2	Q8WZ42	Q8wz42 homo sapien	214	146.5	7.7	484	2	Q9BXN7	Q9bxn7 homo sapien
143	155.5	8.1	332	2	Q9BU81	Q9bu81 homo sapien	215	146.5	7.7	1194	2	Q7TPV3	Q7tpv3 mus musculu
144	155.5	8.1	334	2	Q76PA0	Q76pa0 homo sapien	216	146.5	7.7	1214	2	Q6ZQA6	Q6zqa6 mus musculu
145	155.5	8.1	359	2	P78410	P78410 homo sapien	217	146.5	7.7	362	2	Q9JHQ1	Q9jhq1 rattus norv
146	155.5	8.1	413	2	Q7QBVL	Q7qbl1 anopheles g	218	146	7.7	508	1	FAS3_DROME	P5278 drosophila
147	155.5	8.1	526	1	BUTY_BOVIN	P18892 bos taurus	219	145	7.6	528	2	P91670	P91670 drosophila
148	155	8.1	316	2	Q8VE98	Q8ve98 mus musculu	220	145	7.6	528	2	Q9JLN5	Q9jln5 mus musculu
149	155	8.1	344	1	NTRI_HUMAN	Q9p121 homo sapien	221	144.5	7.6	592	2	Q9JLN5	Q9jln5 mus musculu
150	155	8.1	2012	1	DSCA_HUMAN	Q60469 homo sapien	222	144.5	7.6	697	1	STLA_HUMAN	Q96lc7 homo sapien
151	154	8.1	259	2	Q9Y5B2	Q9y5b2 homo sapien	223	144.5	7.6	858	2	O18466	O18466 hirudo medi
152	154	8.1	394	2	Q7Z499	Q7z499 homo sapien	224	144	7.5	294	2	Q8BH36	Q8bh36 mesocricetu
153	154	8.1	403	2	Q9VP08	Q9vp08 drosophila	225	144	7.5	348	1	NEGR_RAT	Q920j8 rattus norv
154	154	8.1	529	2	Q7TQM3	Q7tqm3 rattus norv	226	144	7.5	384	2	Q8N9I7	Q8n9i7 homo sapien
155	154	8.1	807	2	Q6DD66	Q6dd66 xenopus lae	227	144	7.5	474	2	Q8NFA7	Q8nfaf7 homo sapien
156	154	8.1	818	2	Q91742	Q91742 xenopus lae	228	144	7.5	940	2	O6KD21	O6kdz1 gallus gall
157	154	8.1	818	2	Q9PVS9	Q9psv9 xenopus lae	229	144	7.5	4071	2	P78409	P78409 homo sapien
158	153.5	8.0	321	2	Q6UXI4	Q6uxi4 homo sapien	230	143.5	7.5	731	2	P78409	Q95mi3 bos taurus
159	153	8.0	1340	2	Q8NDA2	Q8nda2 homo sapien	231	143.5	7.5	802	2	Q95MI3	Q90ym1 brachydanio
160	153	8.0	1366	1	ROB3_MOUSE	Q922i4 mus musculu	232	143.5	7.5	838	2	Q90YM1	Q8wv5 homo sapien
161	152.5	8.0	526	1	BUTY_HUMAN	Q13410 homo sapien	233	143	7.5	336	2	Q8WVV5	P32736 rattus norv
162	152.5	8.0	526	2	Q9H458	Q9h458 homo sapien	234	143	7.5	345	1	OPCM_RAT	Q00480 homo sapien
163	152	8.0	315	2	Q6EDM5	Q6edm5 homo sapien	235	143	7.5	523	2	O00480	Q8own2 mus musculu
164	151.5	7.9	738	2	P79390	P79390 bos primige	236	143	7.5	582	2	Q80WN2	Q80wn2 mus musculu
165	151.5	7.9	1093	1	LIG1_HUMAN	Q961a1 homo sapien	237	143	7.5	595	2	Q68SN8	Q68sn8 mus musculu
166	151.5	7.9	1249	2	Q90Z04	Q90z04 xenopus lae	238	143	7.5	739	1	PECL_BOVIN	P22455 homo sapien
167	151	7.9	1228	2	Q8MRA3	Q8mra3 drosophila	239	143	7.5	802	2	Q8TDA0	Q8tda0 homo sapien
168	151	7.9	1675	2	Q8MSW4	Q8msw4 brachydanio	240	143	7.5	802	1	Q8TDA0	Q91743 xenopus lae
169	151	7.9	1906	1	KMLS_CHICK	P11799 gallus gall	241	143	7.5	828	2	Q91743	Q68ev1 xenopus lae
170	150.5	7.9	334	2	Q8NRA4	Q9nr44 homo sapien	242	143	7.5	308	2	Q68EV1	Q6uxi2 homo sapien
171	150.5	7.9	508	2	Q9GLA5	Q961a5 homo sapien	243	142.5	7.5	316	2	Q6UXI2	Q8ifu3 brachydanio
172	150.5	7.9	655	1	LX9_HUMAN	Q9hb97 homo sapien	244	142.5	7.5	351	2	Q8JFU3	Q7sy58 brachydanio
173	150	7.9	316	2	Q7TPB4	Q7tpb4 rattus norv	245	142.5	7.5	351	2	Q7SY58	Q80ul9 mus musculu
174	150	7.9	319	2	O00477	O00477 homo sapien	246	142.5	7.5	379	2	Q80UL9	Q8nc34 homo sapien
175	150	7.9	357	2	O15338	O15338 homo sapien	247	142.5	7.5	388	2	Q8NC34	Q8nb18 homo sapien
176	150	7.9	513	2	O00481	O00481 homo sapien	248	142.5	7.5	534	2	Q8NB18	Q9ttf2 canis famil
177	150	7.9	732	2	Q8CAW4	Q8caw4 mus musculu	249	142.5	7.4	329	2	Q9TTF2	
							250	142					

251	142	7.4	350	2	Q6PJN1	Q6pjnl homo sapien	324	135.5	7.1	1273	2	O44928	O44928 caenorhabdi
252	142	7.4	504	2	Q8N441	Q8n441 homo sapien	325	135.5	7.1	1327	2	Q8QHL3	Q8qhl3 gallus gall
253	142	7.4	504	2	Q9H4D7	Q9h4d7 homo sapien	326	135.5	7.1	1386	1	ROB3_HUMAN	Q9ems0 homo sapien
254	142	7.4	828	2	Q9DGK3	Q9dgk3 xenopus lae	327	135.5	7.1	1428	2	Q8AY67	Q8ay67 brachydanio
255	142	7.4	829	2	Q9PSV8	Q9psv8 xenopus lae	328	135.5	7.1	1662	2	Q7QIV4	Q7qiv4 anopheles g
256	142	7.4	1470	1	ROB2_MOUSE	Q7tpd3 mus musculus	329	135.5	7.1	2133	2	Q7PQ99	Q7pq99 anopheles g
257	141.5	7.4	316	2	Q8BXR1	Q8bxr1 homo sapien	330	135.5	7.1	4736	2	Q7YT99	Q7yt99 mytilus gal
258	141.5	7.4	509	2	Q9EQY5	Q9eqy5 m mman-g pr	331	135	7.1	292	2	Q8OW97	Q8ow97 meriones un
259	141.5	7.4	512	2	Q96DN8	Q96dn8 homo sapien	332	135	7.1	370	2	Q7TSN7	Q7tsn7 mus musculus
260	141.5	7.4	1031	2	Q90YM2	Q90ym2 brachydanio	333	135	7.1	590	1	LIB5_HUMAN	Q75023 homo sapien
261	141	7.4	334	2	Q96AV7	Q96av7 homo sapien	334	135	7.1	621	2	Q811T7	Q811t7 mus musculus
262	141	7.4	352	1	NEGR_HUMAN	Q7z3b1 homo sapien	335	135	7.1	837	1	NCM2_HUMAN	O15394 homo sapien
263	141	7.4	377	2	Q8OV04	Q8ov04 mus musculus	336	135	7.1	1214	2	Q75054	Q75054 homo sapien
264	141	7.4	527	2	Q00475	Q00475 homo sapien	337	134.5	7.0	304	2	Q9BE26	Q9be26 macaca faec
265	141	7.4	536	2	Q8BJE2	Q8bje2 mus musculus	338	134.5	7.0	605	2	Q921F2	Q921f2 mus musculus
266	141	7.4	771	2	Q7QEY8	Q7qey8 anopheles g	339	134.5	7.0	789	1	KIR1_MOUSE	Q80w68 mus musculus
267	141	7.4	822	2	Q91288	Q91288 pleurodeles	340	134.5	7.0	838	2	Q8BQ36	Q8bq36 mus musculus
268	141	7.4	998	2	Q9SR27	Q9sr27 drosophila	341	134.5	7.0	838	2	Q8C4B2	Q8c4b2 mus musculus
269	141	7.4	998	2	Q9W4Y6	Q9w4y6 drosophila	342	134.5	7.0	1060	2	Q9QZ13	Q9qz13 rattus norv
270	140.5	7.4	337	2	Q6DFY2	Q6dfy2 mus musculus	343	134.5	7.0	1091	1	LIG1_MOUSE	Q70193 mus musculus
271	140	7.3	376	2	Q90Z71	Q90z71 brachydanio	344	134	7.0	291	2	Q86FD7	Q86fd7 schistosoma
272	140	7.3	440	2	Q6ZMD4	Q6zmd4 homo sapien	345	134	7.0	297	2	P78408	P78408 homo sapien
273	140	7.3	515	1	PVR1_MOUSE	Q91kf6 mus musculus	346	134	7.0	367	2	Q6ZML4	Q6zml4 homo sapien
274	140	7.3	1051	1	PTK7_CHICK	Q91o48 gallus gall	347	134	7.0	529	2	Q7KYR7	Q7kyr7 homo sapien
275	140	7.3	3198	2	Q9U8G8	Q9u8g8 manduca sex	348	134	7.0	795	2	Q90YMO	Q90ym0 brachydanio
276	139.5	7.3	796	2	Q91287	Q91287 pleurodeles	349	134	7.0	846	2	O57577	O57577 cynops pyr
277	139.5	7.3	1045	2	Q8ET37	Q8et37 homo sapien	350	134	7.0	1100	2	O57576	O57576 cynops pyr
278	139.5	7.3	1197	1	CAM1_BRARE	Q90478 brachydanio	351	134	7.0	2597	2	Q6WRH9	Q6wrh9 rattus norv
279	139.5	7.3	1320	2	Q96KF5	Q96kf5 homo sapien	352	133.5	7.0	285	2	Q9D780	Q9d780 mus musculus
280	139.5	7.3	1320	2	Q8ETC9	Q8etc9 homo sapien	353	133.5	7.0	433	2	Q9V644	Q9v644 drosophila
281	139	7.3	515	2	Q6P9M9	Q6p9m9 mus musculus	354	133.5	7.0	569	1	SILF_MOUSE	Q920g3 mus musculus
282	138.5	7.3	337	1	OPCM_CHICK	Q98892 gallus gall	355	133.5	7.0	1033	2	Q24327	Q24327 drosophila
283	138.5	7.3	344	2	Q6DF61	Q6df61 gallus gall	356	133.5	7.0	1033	2	Q9V643	Q9v643 drosophila
284	138.5	7.3	345	2	Q6QM08	Q6qm08 xenopus lae	357	133.5	7.0	1746	2	Q8WY19	Q8wy19 homo sapien
285	138.5	7.3	853	1	NCA1_BOVIN	P31836 bos taurus	358	133	7.0	289	2	Q8K3J3	Q8k3j3 meriones un
286	138	7.2	344	2	Q9R201	Q9r201 mus musculus	359	133	7.0	650	2	Q63709	Q63709 rattus ep.
287	138	7.2	592	2	Q96KE5	Q96ke5 homo sapien	360	133	7.0	977	2	Q96RD9	Q96rd9 homo sapien
288	138	7.2	1091	1	NCA1_CHICK	P13590 gallus gall	361	133	7.0	1010	1	CONT_CHICK	P14781 gallus gall
289	138	7.2	1099	2	P97527	P97527 rattus norv	362	133	7.0	1036	1	AXO1_CHICK	P28685 gallus gall
290	137.5	7.2	263	2	Q7TPW5	Q7tpw5 mus musculus	363	133	7.0	1333	1	VGR1_MOUSE	P35969 mus musculus
291	137.5	7.2	509	2	Q91PK7	Q91pk7 mus musculus	364	133	7.0	1378	1	ROB2_HUMAN	Q9bck4 homo sapien
292	137.5	7.2	582	2	Q95N25	Q95n25 bos taurus	365	132.5	6.9	980	1	KPMS_FELCA	P13369 felis silve
293	137.5	7.2	697	2	Q922E0	Q922e0 mus musculus	366	132.5	6.9	1994	2	Q6ZPF2	Q6zpp2 mus musculus
294	137.5	7.2	757	1	KIR1_HUMAN	Q96j84 homo sapien	367	132.5	6.9	2176	2	Q6V4S5	Q6v4s5 mus musculus
295	137.5	7.2	789	1	KIR1_RAT	Q6x936 rattus norv	368	132	6.9	296	2	O42404	O42404 gallus gall
296	137.5	7.2	2673	2	Q96SG3	Q96sc3 homo sapien	369	132	6.9	398	2	Q9Y640	Q9y640 homo sapien
297	137	7.2	209	2	Q6DDH9	Q6ddh9 xenopus lae	370	132	6.9	413	2	Q699P0	Q699p0 antherea p
298	137	7.2	283	2	Q8NF70	Q8nf70 homo sapien	371	132	6.9	472	2	Q811T8	Q811t8 mus musculus
299	137	7.2	344	1	CD2_MOUSE	P08920 mus musculus	372	132	6.9	515	2	Q96PJ5	Q96pj5 homo sapien
300	137	7.2	358	2	Q90490	Q90490 brachydanio	373	132	6.9	515	2	Q96RE0	Q96re0 homo sapien
301	137	7.2	421	2	Q7PV30	Q7pv30 anopheles g	374	132	6.9	549	2	Q9NQS3	Q9nqs3 homo sapien
302	137	7.2	1612	1	ROB1_MOUSE	O89026 mus musculus	375	132	6.9	858	2	Q86X47	Q86x47 homo sapien
303	137	7.2	1730	2	Q7YRQ7	Q7yrq7 sus scrofa	376	132	6.9	862	1	CD22_MOUSE	P35329 mus musculus
304	136.5	7.2	336	1	C226_HUMAN	Q15762 homo sapien	377	132	6.9	1026	2	O94780	O94780 homo sapien
305	136.5	7.2	350	2	Q99420	Q99420 homo sapien	378	132	6.9	1030	2	Q8NF48	Q8nf48 homo sapien
306	136.5	7.2	858	1	NCA1_RAT	P13596 rattus norv	379	132	6.9	1100	2	O94779	O94779 homo sapien
307	136.5	7.2	1391	2	Q8N3L4	Q8n3l4 homo sapien	380	132	6.9	1107	2	Q9W0B0	Q9w0b0 drosophila
308	136.5	7.2	1409	2	Q8J127	Q8j127 brachydanio	381	132	6.9	1264	2	P91767	P91767 manduca sex
309	136.5	7.2	1409	2	Q801M2	Q801m2 brachydanio	382	132	6.9	1651	1	ROB1_RAT	O55005 rattus norv
310	136.5	7.2	1614	2	Q8UVD7	Q8uud7 xenopus lae	383	131.5	6.9	416	2	Q8N7I3	Q8n7i3 homo sapien
311	136	7.1	421	2	Q7QLK4	Q7qlk4 anopheles g	384	131.5	6.9	416	2	Q671F8	Q671f8 homo sapien
312	136	7.1	515	1	PVR1_PIG	Q9gl76 sus scrofa	385	131.5	6.9	515	2	Q6EH12	Q6eh12 rattus norv
313	136	7.1	549	2	Q9D006	Q9d006 mus musculus	386	131.5	6.9	779	2	O97136	O97136 manduca sex
314	136	7.1	549	2	Q9JLB9	Q9jlb9 mus musculus	387	131.5	6.9	837	2	O97137	O97137 manduca sex
315	136	7.1	816	2	Q8NFA5	Q8nfa5 homo sapien	388	131.5	6.9	1269	2	O6U7I5	O6u7i5 brachydanio
316	136	7.1	1062	2	Q8BK93	Q8bk93 mus musculus	389	131.5	6.9	1643	2	Q7QG78	Q7qgt8 anopheles g
317	135.5	7.1	487	2	Q7T2H2	Q7t2h2 gallus gall	390	131	6.9	288	2	Q28499	Q28499 macaca mula
318	135.5	7.1	517	1	PVR1_HUMAN	Q15223 homo sapien	391	131	6.9	450	2	Q6UXI0	Q6uxi0 homo sapien
319	135.5	7.1	590	2	Q6P4T5	Q6p4t5 mus musculus	392	131	6.9	725	2	O73634	O73634 xenopus lae
320	135.5	7.1	878	2	Q9GV22	Q9gv22 mytilus gal	393	131	6.9	922	2	O90413	O90413 brachydanio
321	135.5	7.1	1070	1	PTK7_HUMAN	Q13308 homo sapien	394	131	6.9	1028	2	Q6INB5	Q6inb5 xenopus lae
322	135.5	7.1	1070	2	Q6IQ54	Q6iq54 homo sapien	395	131	6.9	1092	1	NCA2_XENLA	P36335 xenopus lae
323	135.5	7.1	1269	2	O01632	O01632 caenorhabdi	396	131	6.9	1254	2	Q674V1	Q674v1 podocoryne

337	131	6.9	1476	2	Q7QJ29	Q7gJ29 anopheles g	470	127	6.7	519	1	ECTO RAT	P16573 rattus norv
338	131	6.9	4391	1	PGBM_HUMAN	P8160 homo sapien	471	127	6.7	591	2	NEO1_HUMAN	Q6np04 drosophila
339	130.5	6.8	390	2	Q66KX2	Q66kx2 xenopus lae	472	127	6.7	595	2	Q6ZRS5	Q6zrs5 homo sapien
340	130.5	6.8	395	2	Q6PSD0	Q6psd0 xenopus. fi	473	127	6.7	784	2	Q8I063	Q8i063 drosophila
401	130.5	6.8	437	2	Q8NFS6	Q8nfs6 homo sapien	474	127	6.7	806	1	CEK2_CHICK	P18406 gallus gall
402	130.5	6.8	480	2	Q8P5D1	Q8p5d1 xenopus. fi	475	127	6.7	1027	2	Q90W79	Q90w79 gallus gall
403	130.5	6.8	482	2	Q90WB5	Q90wb5 anas platyr	476	127	6.7	1316	2	Q7QE16	Q7qe16 anopheles g
404	130.5	6.8	978	1	KFMS_FSVMD	P00545 feline sarc	477	127	6.7	1336	1	VGR1_RAT	P53767 rattus norv
405	130.5	6.8	1125	2	Q7QEC1	Q7qec1 anopheles g	478	127	6.7	1342	2	Q9GPF6	Q9gpp6 drosophila
406	130.5	6.8	2174	2	Q9GQ01	Q9gq01 drosophila	479	127	6.7	1342	2	Q9VPZ7	Q9vpz7 drosophila
407	130	6.8	321	2	Q55202	Q55202 rattus norv	480	127	6.7	1377	1	NEO1_RAT	P97603 rattus norv
408	130	6.8	336	1	C226_MACMU	Q18906 macaca mula	481	127	6.7	1461	1	NEO1_HUMAN	Q92859 homo sapien
409	130	6.8	761	1	NCA2_HUMAN	P13592 homo sapien	482	127	6.7	1651	1	ROB1_HUMAN	Q9y6n7 homo sapien
410	130	6.8	848	1	NCA1_HUMAN	P13591 homo sapien	483	126.5	6.6	315	2	Q8UWL3	Q8uwl3 ictalurus p
411	130	6.8	877	2	Q9GSH3	Q9gsh3 halocynthia	484	126.5	6.6	423	2	Q640R3	Q640r3 mus musculus
412	130	6.8	1946	2	Q68J72	Q68j72 apis mellif	485	126.5	6.6	645	2	Q6NZB6	Q6nzb6 mus musculus
413	129.5	6.8	305	2	Q6DJ75	Q6dj75 xenopus tro	486	126.5	6.6	649	2	Q7TMP7	Q7tmp7 mus musculus
414	129.5	6.8	336	2	Q46551	Q46551 hylobates s	487	126.5	6.6	654	1	LY9_MOUSE	Q01965 mus musculus
415	129.5	6.8	422	2	Q96PJ3	Q96pj3 homo sapien	488	126.5	6.6	733	2	Q8SQ83	Q8sq83 trichosurus
416	129.5	6.8	1499	2	Q90815	Q90815 gallus gall	489	126.5	6.6	1006	2	Q6IDB9	Q6ide9 drosophila
417	129.5	6.8	2217	2	Q9AV57	Q9av57 gallus gall	490	126.5	6.6	2008	2	Q9VEJ5	Q9vej5 drosophila
418	129.5	6.8	5516	2	Q7Z248	Q7z248 brachydanio	491	126.5	6.6	2046	2	Q7KSE9	Q7kse9 drosophila
419	129	6.8	262	2	Q80T70	Q80t70 mus musculus	492	126	6.6	498	2	Q9UBF9	Q9ubf9 homo sapien
420	129	6.8	388	2	Q8R464	Q8r464 mus musculus	493	126	6.6	719	2	Q66IV0	Q66iv0 xenopus lae
421	129	6.8	463	2	Q66J72	Q66j72 xenopus lae	494	126	6.6	725	2	Q73633	Q73633 xenopus lae
422	129	6.8	584	2	Q9Y3V8	Q9y3v8 homo sapien	495	126	6.6	800	2	Q99052	Q99052 mus musculus
423	129	6.8	714	2	Q6ZPE6	Q6zpe6 mus musculus	496	126	6.6	1018	2	Q28106	Q28106 bos taurus
424	129	6.8	1056	2	Q7ZW34	Q7zw34 brachydanio	497	126	6.6	1088	1	NCA1_XENLA	P16170 xenopus lae
425	129	6.8	1117	2	Q6P1C6	Q6plc6 mus musculus	498	126	6.6	1624	2	Q63ZG4	Q63zg4 xenopus lae
426	129	6.8	1338	1	VGR1_HUMAN	P17948 h vascular	499	125.5	6.6	342	2	Q95MM9	Q95mm9 canis famil
427	129	6.8	2828	2	Q9NR99	Q9nr99 homo sapien	500	125.5	6.6	442	2	Q6KAT6	Q6kat6 mus musculus
428	128.5	6.7	280	2	Q9TTF1	Q9ttf1 canis famil	501	125.5	6.6	493	2	Q6PSY4	Q6psy4 homo sapien
429	128.5	6.7	285	2	Q8VE93	Q8ve93 mus musculus	502	125.5	6.6	525	2	Q7PZS8	Q7pzs8 anopheles g
430	128.5	6.7	332	1	SUF6_HUMAN	Q6edu3 homo sapien	503	125.5	6.6	975	1	KIT_MOUSE	P05532 mus musculus
431	128.5	6.7	452	2	Q70355	Q70355 mus musculus	504	125.5	6.6	975	2	Q6QJB7	Q6qjb7 mus musculus
432	128.5	6.7	480	2	Q9PSC9	Q9psc9 xenopus. fi	505	125.5	6.6	975	2	Q6QJB8	Q6qjb8 mus musculus
433	128.5	6.7	508	2	Q8BJA5	Q8bjas mus musculus	506	125	6.6	402	1	RAGE_RAT	Q63495 rattus norv
434	128.5	6.7	521	2	Q61352	Q61352 mus musculus	507	125	6.6	402	2	Q6MG86	Q6mg86 rattus norv
435	128.5	6.7	727	2	Q6KRB2	Q6krb2 rattus norv	508	125	6.6	570	2	Q8NCF6	Q8nce6 homo sapien
436	128.5	6.7	813	1	FOR2_XENLA	Q03364 xenopus lae	509	125	6.6	627	2	Q8N466	Q8n466 homo sapien
437	128.5	6.7	814	2	Q6GNP8	Q6gnp8 xenopus lae	510	125	6.6	705	2	Q8CBD3	Q8cbd3 mus musculus
438	128.5	6.7	837	2	Q6RKB3	Q6rkb3 rattus norv	511	125	6.6	782	2	Q61563	Q61563 mus musculus
439	128.5	6.7	1302	1	NRG_DROME	P20241 drosophila	512	125	6.6	800	2	Q7TSI8	Q7tsi8 mus musculus
440	128.5	6.7	17903	2	Q7RTL4	Q7rtl4 drosophila	513	125	6.6	801	1	FR3_MOUSE	Q61851 mus musculus
441	128	6.7	285	2	Q8BTK0	Q8btk0 mus musculus	514	125	6.6	898	2	Q69Z26	Q69z26 mus musculus
442	128	6.7	288	2	Q77684	Q77684 macaca neme	515	125	6.6	1018	1	CONT_HUMAN	Q12860 homo sapien
443	128	6.7	316	2	Q9AW77	Q9aw77 brachydanio	516	125	6.6	2772	2	Q9VAV4	Q9vav4 drosophila
444	128	6.7	381	2	Q9Y4A4	Q9y4a4 homo sapien	517	125	6.6	2894	2	Q7KRX2	Q7kxr2 drosophila
445	128	6.7	454	2	Q6MG97	Q6mg97 rattus norv	518	124.5	6.5	303	2	Q7ZXR4	Q7zxr4 xenopus lae
446	128	6.7	643	1	LIB5_PANTR	Q8mjz7 pan troglod	519	124.5	6.5	310	1	FCGB_HUMAN	P31994 homo sapien
447	128	6.7	762	2	Q71TW8	Q71tw8 homo sapien	520	124.5	6.5	321	2	Q6INF0	Q6info xenopus lae
448	128	6.7	800	2	Q9JHX9	Q9jhx9 rattus norv	521	124.5	6.5	342	2	P97635	P97635 rattus norv
449	128	6.7	837	2	Q7Z7F2	Q7z7f2 homo sapien	522	124.5	6.5	392	2	Q7PSN2	Q7psn2 anopheles g
450	128	6.7	1501	2	Q7TTL7	Q7ttl7 mus musculus	523	124.5	6.5	632	2	Q6ZRX5	Q6zrx5 homo sapien
451	128	6.7	1501	2	Q9QW00	Q9qw00 rattus sp.	524	124.5	6.5	662	2	Q8MQZ9	Q8mqz9 drosophila
452	128	6.7	1863	2	Q64605	Q64605 rattus norv	525	124.5	6.5	662	2	Q9VGD0	Q9vgd0 drosophila
453	128	6.7	1904	2	Q64699	Q64699 mus musculus	526	124.5	6.5	671	2	Q63711	Q63711 rattus ratt
454	128	6.7	2213	2	Q7Z5N4	Q7z5n4 mus musculus	527	124.5	6.5	725	1	NCA2_MOUSE	P13594 mus musculus
455	127.5	6.7	91	2	Q91667	Q91667 xenopus lae	528	124.5	6.5	764	2	Q8MQQ1	Q8mqql drosophila
456	127.5	6.7	232	2	Q7PJ18	Q7pj18 anopheles g	529	124.5	6.5	785	2	Q9W4U1	Q9w4ul drosophila
457	127.5	6.7	288	1	CD80_HUMAN	P33681 homo sapien	530	124.5	6.5	814	2	O8AYP3	O8ayp3 brachydanio
458	127.5	6.7	385	2	Q9UQF5	Q9uqf5 homo sapien	531	124.5	6.5	972	1	KFMS_HUMAN	P07333 homo sapien
459	127.5	6.7	398	2	Q8N126	Q8n126 homo sapien	532	124.5	6.5	975	2	Q7TS86	Q7ts86 mus musculus
460	127.5	6.7	404	2	Q93IE9	Q93ie9 homo sapien	533	124.5	6.5	1020	1	CONT_MOUSE	P12960 mus musculus
461	127.5	6.7	416	1	RAGE_BOVIN	Q28173 bos taurus	534	124.5	6.5	1020	2	Q6NXV7	Q6nxv7 mus musculus
462	127.5	6.7	432	2	Q9UJF1	Q9ujf1 homo sapien	535	124.5	6.5	1028	2	Q62682	Q62682 rattus norv
463	127.5	6.7	455	2	Q9UIR0	Q9uir0 homo sapien	536	124.5	6.5	1115	1	NCA1_MOUSE	P13595 mus musculus
464	127.5	6.7	499	1	L1A4_HUMAN	P59901 homo sapien	537	124	6.5	193	2	Q7QGF6	Q7qgt6 anopheles g
465	127.5	6.7	510	2	Q7L3E0	Q7l3e0 homo sapien	538	124	6.5	367	2	Q9D4M0	Q9d4m0 mus musculus
466	127.5	6.7	524	2	Q92IK7	Q92ik7 mus musculus	539	124	6.5	372	2	Q8C257	Q8c257 mus musculus
467	127.5	6.7	772	2	Q9Y2J6	Q9y2j6 homo sapien	540	124	6.5	467	1	SIL5_MOUSE	Q91y57 mus musculus
468	127.5	6.7	1028	2	P97528	P97528 rattus norv	541	124	6.5	498	2	Q8BRT6	Q8brt6 mus musculus
469	127	6.7	464	2	Q6GL25	Q6gl25 xenopus tro	542	124	6.5	537	1	IR18_MOUSE	Q61098 mus musculus

543	124	6.5	731	2	Q91150	Q91150 notophthalm	616	121	6.3	173	2	Q9JKD5	Q9jkd5 rattus norv
544	124	6.5	817	2	Q8UG38	Q8jg38 brachydanio	617	121	6.3	304	2	Q9TX1	Q9tcx1 canis famil
545	124	6.5	837	1	NCM2_MOUSE	O35136 mus musculus	618	121	6.3	305	2	Q98261	Q98261 homo sapien
546	124	6.5	880	2	Q7KPO8	Q7kpg8 drosophila	619	121	6.3	328	2	Q6FHAB	Q6fhab oncorhynch
547	124	6.5	1026	2	Q62845	Q62845 rattus norv	620	121	6.3	365	2	Q8AXL6	Q8axl6 mus musculus
548	124	6.5	1395	2	Q7KVK3	Q7kvk3 drosophila	621	121	6.3	523	2	Q8K2H7	Q8k2h7 mus musculus
549	124	6.5	1429	2	Q9W213	Q9w213 drosophila	622	121	6.3	537	2	Q7PSU8	Q7psu8 anopheles g
550	124	6.5	2776	2	Q869A0	Q869a0 drosophila	623	121	6.3	601	2	Q96CU3	Q96cu3 homo sapien
551	124	6.5	2898	2	Q868Z9	Q868z9 drosophila	624	121	6.3	740	1	PEC1_PIG	Q5242 sus scrofa
552	124	6.5	4001	2	Q9N2P7	Q9n2p7 drosophila	625	121	6.3	841	2	Q8R2Z1	Q8r2z1 mus musculus
553	123.5	6.5	325	2	Q8HW98	Q8hw98 mus musculus	626	121	6.3	965	2	Q86BP9	Q86bp9 drosophila
554	123.5	6.5	396	2	Q9WN28	Q9wn28 m nectin-li	627	121	6.3	1009	2	O31250	Q93250 xenopus lae
555	123.5	6.5	461	2	Q13854	Q13854 homo sapien	628	121	6.3	1062	2	Q960C4	Q960c4 drosophila
556	123.5	6.5	531	2	Q7QEV7	Q7qev7 anopheles g	629	121	6.3	1062	2	Q7IZ99	Q7iz99 drosophila
557	123.5	6.5	979	2	Q8C8K9	Q8c8k9 mus musculus	630	121	6.3	1252	2	Q9JL11	Q9jl11 mus musculus
558	123.5	6.5	1513	2	Q9OZ70	Q9oz70 brachydanio	631	121	6.3	1389	2	Q90Z69	Q90z69 brachydanio
559	123.5	6.5	1860	2	Q7POF4	Q7pqf4 anopheles g	632	121	6.3	1419	2	Q98SW3	Q98sw3 brachydanio
560	123.5	6.5	1948	1	PTNS_HUMAN	Q13332 homo sapien	633	121	6.3	1914	2	O724J0	Q724j0 homo sapien
561	123	6.4	282	2	Q9Y639	Q9y639 homo sapien	634	121	6.3	6620	2	Q96AA2	Q96aa2 homo sapien
562	123	6.4	366	2	Q6NV23	Q6nv23 homo sapien	635	120.5	6.3	281	2	P97300	P97300 mus musculus
563	123	6.4	403	2	Q8HY15	Q8hy15 lemur catta	636	120.5	6.3	395	2	Q8BXJ7	Q8bxj7 m mus muscu
564	123	6.4	417	2	Q7TNL1	Q7tnl1 mus musculus	637	120.5	6.3	395	2	Q8BZP4	Q8bzp4 mus musculus
565	123	6.4	496	2	Q9JIF9	Q9jif9 mus musculus	638	120.5	6.3	404	2	Q8BLO9	Q8blo9 mus musculus
566	123	6.4	520	2	Q925P2	Q925p2 mus musculus	639	120.5	6.3	404	2	O8BYPL	O8bypl mus musculus
567	123	6.4	729	2	Q91147	Q91147 notophthalm	640	120.5	6.3	822	2	Q9QV77	Q9qv77 rattus sp.
568	123	6.4	800	2	Q86LF9	Q86lf9 drosophila	641	120.5	6.3	1052	2	Q7PMY4	Q7pmy4 anopheles g
569	123	6.4	801	2	Q86LF8	Q86lf8 drosophila	642	120.5	6.3	1150	2	Q8BS24	Q8bs24 mus musculus
570	123	6.4	1028	2	Q8C6X1	Q8c6x1 mus musculus	643	120.5	6.3	1209	2	P70232	P70232 mus musculus
571	123	6.4	1028	2	Q9JMB8	Q9jmb8 mus musculus	644	120.5	6.3	1276	2	Q90X22	Q90x22 brachydanio
572	123	6.4	1395	2	O44924	O44924 drosophila	645	120	6.3	288	2	Q9TT70	Q9tt70 sus scrofa
573	123	6.4	1596	2	Q9HCL6	Q9hcl6 homo sapien	646	120	6.3	297	2	Q9BE99	Q9be99 sus scrofa
574	123	6.4	2212	2	Q9NHN3	Q9nhn3 homo sapien	647	120	6.3	321	2	O35187	O35187 rattus norv
575	123	6.4	4796	2	Q9W055	Q9w055 drosophila	648	120	6.3	330	1	CD86_RABIT	P42071 cryptotolagus
576	123	6.4	4796	2	Q9NFS3	Q9nfs3 drosophila	649	120	6.3	388	2	Q8NFZ8	Q8nfz8 homo sapien
577	123	6.4	16215	2	Q9NFS3	Q9nfs3 drosophila	650	120	6.3	420	2	O68DM9	O68dm9 homo sapien
578	122.5	6.4	18074	2	Q917U4	Q917u4 drosophila	651	120	6.3	442	2	Q9H8B3	Q9h8b3 homo sapien
579	122.5	6.4	305	2	Q9VIM2	Q9vim2 mus musculus	652	120	6.3	521	1	CEA1_MOUSE	P31809 mus musculus
580	122.5	6.4	342	2	Q95L99	Q95l99 canis famil	653	120	6.3	521	2	Q925P3	Q925p3 mus musculus
581	122.5	6.4	481	2	Q8MJZ2	Q8mjz2 pan troglod	654	120	6.3	702	1	CEA5_HUMAN	P06731 homo sapien
582	122.5	6.4	499	1	SIL8_HUMAN	Q9nyz4 homo sapien	655	120	6.3	702	2	Q8N4D0	Q8n4d0 homo sapien
583	122.5	6.4	538	2	Q9NWQ7	Q9nwq7 homo sapien	656	120	6.3	769	2	O8N115	O8n115 homo sapien
584	122.5	6.4	821	1	FGR2_MOUSE	P18033 mus musculus	657	120	6.3	806	1	FGR3_HUMAN	P22607 homo sapien
585	122.5	6.4	1028	2	Q9UQ52	Q9uq52 homo sapien	658	120	6.3	841	2	P97484	P97484 mus musculus
586	122.5	6.4	1694	1	SN_MOUSE	Q9w675 brachydanio	659	120	6.3	1040	1	AXO1_HUMAN	Q02246 homo sapien
587	122	6.4	352	2	Q9W6V2	Q9w6v2 mus musculus	660	120	6.3	1043	2	Q6PA07	P22063 rattus norv
588	122	6.4	496	2	Q7Z0T5	Q7z0t5 gallus gall	661	120	6.3	1388	2	O7QKD0	Q7qkd0 anopheles lae
589	122	6.4	540	2	Q8N0Z9	Q8n0z9 homo sapien	662	120	6.3	1388	2	O7QKD0	Q7qkd0 anopheles g
590	122	6.4	697	2	Q8TC35	Q8tc35 homo sapien	663	120	6.3	1914	1	KMLS_HUMAN	O15746 homo sapien
591	122	6.4	821	1	FGR2_HUMAN	P21802 homo sapien	664	119.5	6.3	276	2	Q840S5	Q840s5 xenopus tro
592	122	6.4	972	2	Q86VW7	Q86vw7 homo sapien	665	119.5	6.3	333	1	C226_MOUSE	Q8k4f0 mus musculus
593	122	6.4	1026	2	Q81WV2	Q81wv2 homo sapien	666	119.5	6.3	388	1	BASI_CHICK	P17790 gallus gall
594	122	6.4	1086	2	Q7OH02	Q7oh02 anopheles g	667	119.5	6.3	399	2	Q6MG94	Q6mg94 rattus norv
595	122	6.4	1187	2	Q8WR45	Q8wr45 caenorhabdi	668	119.5	6.3	428	2	O6F3J3	O6f3j3 mus musculus
596	122	6.4	4796	2	Q9NL88	Q9nl88 drosophila	669	119.5	6.3	631	1	LIB3_HUMAN	O75022 homo sapien
597	121.5	6.4	240	1	C048_MOUSE	P18181 mus musculus	670	119.5	6.3	707	2	Q9TT07	Q9tt07 canis famil
598	121.5	6.4	240	1	Q6P905	Q6p905 mus musculus	671	119.5	6.3	733	2	Q6O830	Q6o830 mus musculus
599	121.5	6.4	278	2	Q9OYL3	Q9oyl3 mus musculus	672	119.5	6.3	733	2	Q9QZM7	Q9qzm7 mus musculus
600	121.5	6.4	291	2	Q8UVA7	Q8uva7 brachydanio	673	119.5	6.3	782	2	Q9TTZ3	Q9ttz3 cryptotolagus
601	121.5	6.4	336	2	Q8WNV8	Q8wnv8 felis silve	674	119.5	6.3	819	1	FGR1_CHICK	P21804 gallus gall
602	121.5	6.4	390	2	Q9H1X9	Q9hlx9 homo sapien	675	119.5	6.3	822	1	FGR1_RAT	Q04589 rattus norv
603	121.5	6.4	393	2	Q97547	P97547 rattus norv	676	119.5	6.3	822	2	Q6O818	Q6o818 mus musculus
604	121.5	6.4	468	2	Q6PJ50	Q6pj50 mus musculus	677	119.5	6.3	1406	2	Q9VQP7	Q9vqp7 drosophila
605	121.5	6.4	499	2	Q7Z728	Q7z728 homo sapien	678	119.5	6.3	1463	2	Q9VQ08	Q9vq08 drosophila
606	121.5	6.4	524	1	BUTY_MOUSE	Q62556 mus musculus	679	119.5	6.3	6632	1	UN89_CAEEL	O01761 caenorhabdi
607	121.5	6.4	544	2	Q8C2D4	Q8c2d4 mus musculus	680	119.5	6.3	8081	2	O721Z0	O721z0 caenorhabdi
608	121.5	6.4	611	2	Q70W32	Q70w32 oncorhynch	681	119	6.2	290	2	Q62680	Q62680 rattus norv
609	121.5	6.4	827	2	Q6GNS5	Q6gns5 xenopus lae	682	119	6.2	321	2	Q62624	Q62624 rattus norv
610	121.5	6.4	948	2	Q9TTD7	Q9tttd7 trichosurus	683	119	6.2	328	2	O15430	O15430 homo sapien
611	121.5	6.4	1021	1	CONT_RAT	Q63198 rattus norv	684	119	6.2	401	2	Q7PSS8	Q7ps8 anopheles g
612	121.5	6.4	1443	2	Q8MTB2	Q8mtb2 drosophila	685	119	6.2	550	2	Q9VMN9	Q9vmn9 drosophila
613	121.5	6.4	1765	2	Q9VS30	Q9vs30 drosophila	686	119	6.2	640	2	O8BSM2	O8bsm2 mus musculus
614	121.5	6.4	1770	2	Q9VSD9	Q9vsd9 drosophila	687	119	6.2	675	2	Q7OV55	Q7ov55 xenopus lae
615	121.5	6.4	1827	2	Q9VSG5	Q9vsg5 drosophila	688	119	6.2	749	2	Q967D9	Q967d9 drosophila

689	119	6.2	823	1	CEK3_CHICK	P18461 gallus gall	762	117	6.1	898	1	FAS2_SCHAM	P22648 schistocerc
690	119	6.2	902	2	Q8IQ17	Q8iql7 drosophila	763	117	6.1	907	2	Q9NEG0	Q9neg0 drosophila
691	119	6.2	903	2	Q967D8	Q967d8 drosophila	764	117	6.1	939	2	Q967X6	Q967x6 drosophila
692	119	6.2	903	2	Q9VQV1	Q9vqv1 drosophila	765	117	6.1	939	2	Q9VB35	Q9vb35 drosophila
693	119	6.2	1028	2	Q07409	Q07409 mus musculus	766	117	6.1	1040	1	AXO1_MOUSE	Q61330 mus musculus
694	119	6.2	1106	2	Q8WX93	Q8wx93 homo sapien	767	117	6.1	1155	2	Q7Q3K8	Q7qz3k8 anopheles g
695	119	6.2	1508	2	Q6NR34	Q6nr34 drosophila	768	117	6.1	3215	2	Q8IRV7	Q8irv7 drosophila
696	119	6.2	1508	2	Q9VQZ2	Q9vqz2 drosophila	769	117	6.1	4117	2	Q8IRV9	Q8irv9 drosophila
697	119	6.2	1531	2	Q967D7	Q967d7 drosophila	770	117	6.1	4179	2	Q9W4Y4	Q9w4y4 drosophila
698	118.5	6.2	281	2	P97546	P97546 rattus norv	771	117	6.1	4223	2	Q8MPN3	Q8mpn3 drosophila
699	118.5	6.2	306	2	Q9R129	Q9r129 mus musculus	772	117	6.1	4228	2	Q8IRV8	Q8irv8 drosophila
700	118.5	6.2	330	1	Q6QP58	Q6qp58 canis famil	773	117	6.1	18412	2	Q7ZZ61	Q7zz61 brachydanio
701	118.5	6.2	344	1	CEA6_HUMAN	P40199 homo sapien	774	116.5	6.1	280	2	Q8UV51	Q8uv51 brachydanio
702	118.5	6.2	344	2	Q13774	Q13774 homo sapien	775	116.5	6.1	324	2	Q8UV72	Q8uv72 brachydanio
703	118.5	6.2	379	2	Q9CWM1	Q9cwm1 mus musculus	776	116.5	6.1	339	1	Q8WMI8	Q8wmi8 homo sapien
704	118.5	6.2	487	2	Q6Q4G2	Q6q4g2 gallus gall	777	116.5	6.1	417	1	PVR_CERAE	P32506 cercopithec
705	118.5	6.2	492	2	Q9ET54	Q9et54 mus musculus	778	116.5	6.1	729	2	Q63827	Q63827 rattus norv
706	118.5	6.2	731	2	Q8CFK8	Q8cfk8 mus musculus	779	116.5	6.1	761	2	Q95LQ2	Q95lq2 macaca fasc
707	118.5	6.2	733	2	Q8OT10	Q8ot10 mus musculus	780	116.5	6.1	810	2	Q7PUH1	Q7puh1 anopheles g
708	118.5	6.2	737	2	Q965M3	Q965m3 caenorhabdi	781	116.5	6.1	816	2	Q91285	Q91285 pleurodeles
709	118.5	6.2	764	1	ICCR_DROME	Q8i80 drosophila	782	116.5	6.1	1465	2	Q7TQ85	Q7tq85 mus musculus
710	118.5	6.2	820	2	Q8CIN9	Q8cim9 mus musculus	783	116.5	6.1	2022	2	Q7KQO5	Q7kqo5 drosophila
711	118.5	6.2	822	1	FGR1_HUMAN	P11362 homo sapien	784	116.5	6.1	2995	2	Q696W0	Q696w0 brachydanio
712	118.5	6.2	822	1	FGR1_MOUSE	P16092 mus musculus	785	116	6.1	241	2	Q6SYC2	Q6sync2 homo sapien
713	118.5	6.2	853	2	Q6DFX7	Q6dfx7 mus musculus	786	116	6.1	312	2	Q66KV0	Q66kv0 xenopus lae
714	118.5	6.2	881	2	Q965M2	Q965m2 caenorhabdi	787	116	6.1	328	2	Q6ZMC9	Q6zmc9 homo sapien
715	118.5	6.2	1081	2	Q99ZT7	Q99zt7 mus musculus	788	116	6.1	370	1	C244_HUMAN	Q9bzw8 homo sapien
716	118.5	6.2	1328	2	Q21043	Q21043 caenorhabdi	789	116	6.1	391	2	Q7T1J4	Q7t1j4 brachydanio
717	118.5	6.2	1415	2	Q94155	Q94155 caenorhabdi	790	116	6.1	458	2	Q61351	Q61351 mus musculus
718	118.5	6.2	1447	2	Q16779	Q16779 caenorhabdi	791	116	6.1	538	2	Q8C9E4	Q8c9e4 mus musculus
719	118.5	6.2	1493	1	NSO1_MOUSE	P97798 mus musculus	792	116	6.1	551	2	Q8MSN7	Q8msn7 drosophila
720	118.5	6.2	8625	2	Q86GD6	Q86gd6 procambarus	793	116	6.1	620	2	Q9HCN6	Q9hcn6 homo sapien
721	118	6.2	423	2	Q8BU57	Q8bu57 mus musculus	794	116	6.1	785	2	Q7TNP4	Q7tnp4 mus musculus
722	118	6.2	510	2	Q8O1V8	Q8o1v8 brachydanio	795	116	6.1	956	2	Q9W4T9	Q9w4t9 drosophila
723	118	6.2	705	2	Q63710	Q63710 rattus ratt	796	116	6.1	959	2	Q9N9Y9	Q9n9y9 drosophila
724	118	6.2	723	2	Q86Y14	Q86y14 homo sapien	797	116	6.1	975	2	Q97174	Q97174 drosophila
725	118	6.2	802	2	Q42127	Q42127 xenopus lae	798	116	6.1	1026	2	Q7Q651	Q7q651 anopheles g
726	118	6.2	815	2	Q8O5B9	Q8o5b9 brachydanio	799	116	6.1	1102	2	Q923W7	Q923w7 mus musculus
727	118	6.2	1109	2	Q8CE91	Q8ce91 mus musculus	800	116	6.1	1109	2	Q6P5H3	Q6p5h3 mus musculus
728	118	6.2	1110	2	Q8CEY3	Q8cey3 mus musculus	801	116	6.1	1109	2	Q6AZB0	Q6azb0 mus musculus
729	118	6.2	1283	2	Q8LIW4	Q8liw4 oryza sativ	802	116	6.1	4816	2	Q8T1O3	Q8t1o3 bombyx mori
730	118	6.2	1502	2	Q3UM81	Q3um81 homo sapien	803	115.5	6.1	292	2	Q6UY47	Q6uy47 homo sapien
731	118	6.2	19066	2	Q8O1W8	Q8o1w8 brachydanio	804	115.5	6.1	323	3	FCGC_HUMAN	P31995 homo sapien
732	117.5	6.2	327	2	Q9UV63	Q9uv63 brachydanio	805	115.5	6.1	345	2	Q9UIE8	Q9uib8 homo sapien
733	117.5	6.2	385	1	BASI_HUMAN	P35613 h basigin p	806	115.5	6.1	492	2	Q8C0U8	Q8c0u8 mus musculus
734	117.5	6.2	533	2	Q9DEE1	Q9dee1 gallus gall	807	115.5	6.1	634	2	Q7RW50	Q7rwb0 neurospora
735	117.5	6.2	533	2	Q3DEE5	Q9dee5 gallus gall	808	115.5	6.1	636	2	Q22040	Q22040 caenorhabdi
736	117.5	6.2	600	2	Q9N7W7	Q9n7w7 homo sapien	809	115.5	6.1	834	2	Q6DCD2	Q6dcd2 xenopus lae
737	117.5	6.2	707	2	Q7PWJ1	Q7pwj1 anopheles g	810	115.5	6.1	1114	2	Q9BWV1	Q9bvw1 homo sapien
738	117.5	6.2	1225	2	Q6GP61	Q6gp61 xenopus lae	811	115.5	6.1	1115	2	Q6UXJ5	Q6uxj5 homo sapien
739	117.5	6.2	1234	1	NPHN_RAT	Q9f044 rattus norv	812	115.5	6.1	1253	2	Q9EQS8	Q9eqs8 mus musculus
740	117.5	6.2	1252	2	Q9JIX2	Q9jix2 rattus norv	813	115	6.0	275	2	Q9JK39	Q9jk39 mus musculus
741	117.5	6.2	1721	2	Q961U1	Q961u1 drosophila	814	115	6.0	335	2	Q9NYO8	Q9nyo8 homo sapien
742	117.5	6.2	2403	2	Q8MLD5	Q8mld5 drosophila	815	115	6.0	377	2	Q9VQY0	Q9vqy0 drosophila
743	117.5	6.2	4463	2	Q8MLD8	Q8mld8 drosophila	816	115	6.0	506	2	Q82D70	Q82d70 streptomyce
744	117.5	6.2	6658	2	Q76281	Q76281 drosophila	817	115	6.0	605	2	Q9VMN6	Q9vmn6 drosophila
745	117.5	6.2	7210	2	Q9V7G8	Q9v7g8 drosophila	818	115	6.0	619	2	Q7PX10	Q7pxi0 anopheles g
746	117.5	6.2	8647	2	Q7KQP5	Q7kqp5 drosophila	819	115	6.0	1066	2	Q8MSR5	Q8msr5 drosophila
747	117.5	6.2	8648	2	Q7KQP6	Q7kqp6 drosophila	820	115	6.0	1479	2	Q7KQT5	Q7kqt5 drosophila
748	117.5	6.2	8930	2	Q7KQP7	Q7kqp7 drosophila	821	115	6.0	1933	2	Q6V3A4	Q6v3a4 mus musculus
749	117.5	6.2	8943	2	Q9V4F7	Q9v4f7 drosophila	822	115	6.0	2159	2	Q6PAL2	Q6pal2 mus musculus
750	117.5	6.2	9270	2	Q8MLD9	Q8mld9 drosophila	823	114.5	6.0	143	2	Q7Z3W0	Q7z3w0 homo sapien
751	117	6.1	244	2	Q75871	Q75871 homo sapien	824	114.5	6.0	321	2	Q8UVA9	Q8uv49 brachydanio
752	117	6.1	244	2	Q3715	Q03715 homo sapien	825	114.5	6.0	330	2	Q6PEU7	Q6peu7 mus musculus
753	117	6.1	261	2	Q9W6V1	Q9w6v1 gallus gall	826	114.5	6.0	412	2	Q8HY14	Q8hy14 cryotolagus
754	117	6.1	265	2	Q8IPG9	Q8ipg9 drosophila	827	114.5	6.0	475	2	Q96PL5	Q96pl5 homo sapien
755	117	6.1	289	2	Q9QYL5	Q9qyl5 mus musculus	828	114.5	6.0	521	2	Q8BHA1	Q8bha1 m mus muscu
756	117	6.1	298	2	Q961I4	Q96i14 drosophila	829	114.5	6.0	530	1	PVR2_MOUSE	P32507 mus musculus
757	117	6.1	360	2	Q8MRE6	Q8mre6 drosophila	830	114.5	6.0	530	2	Q8OXJ5	Q8oxj5 mus musculus
758	117	6.1	399	2	Q7QCH7	Q7qch7 anopheles g	831	114.5	6.0	562	2	Q6YNR7	Q6ynr7 brachydanio
759	117	6.1	467	2	Q8C6F2	Q8c6f2 mus musculus	832	114.5	6.0	626	1	MAG_HUMAN	P20916 homo sapien
760	117	6.1	620	1	SNP_COTJA	Q92154 coturnix co	833	114.5	6.0	631	2	Q8MJZ3	Q8mjz3 pan troglod
761	117	6.1	800	2	Q918X3	Q918x3 brachydanio	834	114.5	6.0	719	2	Q9U4G1	Q9u4g1 drosophila



835	114.5	6.0	956	1	MDC1_HUMAN	Q72553	homo sapien	908	112.5	5.9	3347	2	Q8MMJ9	Q8mmj9	bombyx mori
836	114.5	6.0	978	1	KIT_FELCA	Q28889	felis silve	909	112.5	5.9	3354	2	Q8T101	Q8t101	bombyx mori
837	114.5	6.0	1056	2	Q90Z03	Q90z03	xenopus lae	910	112	5.9	248	1	MYPO_MOUSE	P27573	mus musculus
838	114.5	6.0	838	1	Q9TXI8	Q9txi8	caenorhabdi	911	112	5.9	275	2	Q6PH44	Q6ph44	brachydanio
839	114.5	6.0	1073	2	P79701	P79701	coturnix co	912	112	5.9	282	2	Q8VIM1	Q8vim1	mus musculus
840	114.5	6.0	2224	2	Q9ULM1	Q9ulm1	drosophila	913	112	5.9	283	2	Q8K091	Q8k091	mus musculus
841	114.5	6.0	4824	2	Q95YM1	Q95ym1	procambarus	914	112	5.9	287	2	Q13984	Q13984	homo sapien
842	114.5	6.0	17352	2	Q95YM2	Q95ym2	procambarus	915	112	5.9	288	2	Q9BDN6	Q9bdn6	cercocobus
843	114	6.0	378	2	Q66MN4	Q66mn4	petromyzon	916	112	5.9	289	2	Q28347	Q28347	cercocobus
844	114	6.0	402	2	Q35444	Q35444	mus musculus	917	112	5.9	295	2	Q922H8	Q922h8	mus musculus
845	114	6.0	424	2	Q8C6W0	Q8c6w0	mus musculus	918	112	5.9	340	2	Q61349	Q61349	mus musculus
846	114	6.0	458	2	Q63093	Q63093	rattus norv	919	112	5.9	445	2	Q8R4L1	Q8r4l1	mus musculus
847	114	6.0	468	2	Q9BX59	Q9bx59	homo sapien	920	112	5.9	476	2	Q6AYP5	Q6ayp5	rattus norv
848	114	6.0	468	2	Q9NWB8	Q9nwb8	homo sapien	921	112	5.9	1092	2	Q91ZT0	Q91zt0	rattus norv
849	114	6.0	538	2	Q28939	Q28939	sus scrofa	922	112	5.9	1343	1	VGR2_RAT	Q08775	rattus norv
850	114	6.0	538	2	Q29123	Q29123	sus scrofa	923	112	5.9	1363	2	Q91ZT1	Q91zt1	rattus norv
851	114	6.0	826	2	Q7Q1P7	Q7q1p7	anopheles g	924	112	5.9	1395	2	Q7QBG0	Q7qbg0	anopheles g
852	114	6.0	946	2	Q07153	Q07153	torpedo cal	925	112	5.9	2029	1	LAR_DROME	P16621	drosophila
853	114	6.0	953	2	Q8P6Y9	Q8p6y9	xenopus lae	926	111.5	5.8	215	1	CIB3_MACFA	Q8bxj7	macaca faec
854	114	6.0	1482	2	Q9V4Y0	Q9v4y0	drosophila	927	111.5	5.8	235	2	Q9N0T0	Q9n0t0	canis fami
855	114	6.0	2222	2	Q7QEG7	Q7qeg7	anopheles g	928	111.5	5.8	235	2	Q9TQ88	Q9tq88	canis fami
856	114	6.0	3375	1	UN52_CABEL	Q06561	caenorhabdi	929	111.5	5.8	285	2	Q7ZY30	Q7zy30	xenopus lae
857	113.5	5.9	163	2	Q9NVJ5	Q9nvj5	homo sapien	930	111.5	5.8	306	1	CD80_MOUSE	Q00609	mus musculus
858	113.5	5.9	307	2	Q5A947	Q5a947	rattus norv	931	111.5	5.8	309	2	Q91VY7	Q91yv7	mus musculus
859	113.5	5.9	382	2	Q7PSH7	Q7psh7	anopheles g	932	111.5	5.8	317	2	Q9ESA3	Q9esa3	rattus norv
860	113.5	5.9	465	2	Q640J0	Q640j0	xenopus lae	933	111.5	5.8	331	2	Q9IB01	Q9ib01	spherooides
861	113.5	5.9	487	2	Q6Q4G0	Q6q4g0	gallus gall	934	111.5	5.8	342	2	Q9ESA1	Q9esa1	rattus norv
862	113.5	5.9	487	2	Q6Q4V7	Q6q4v7	gallus gall	935	111.5	5.8	400	2	Q8HY16	Q8hy16	cebus apell
863	113.5	5.9	487	2	Q9W6V7	Q9w6v7	gallus gall	936	111.5	5.8	401	2	Q08835	Q08835	cercopithec
864	113.5	5.9	576	2	Q8MYR8	Q8myr8	drosophila	937	111.5	5.8	403	1	RAGE_MOUSE	Q62151	mus musculus
865	113.5	5.9	743	2	Q8R6B2	Q8r6b2	vibriophage	938	111.5	5.8	417	1	PVR_HUMAN	P15151	homo sapien
866	113.5	5.9	803	2	Q80ZF5	Q80zf5	rattus norv	939	111.5	5.8	446	2	Q6CQ08	Q6qc08	kluyveromyc
867	113.5	5.9	920	2	Q9P232	Q9p232	homo sapien	940	111.5	5.8	446	2	Q9Y849	Q9y849	kluyveromyc
868	113.5	5.9	1098	2	Q961D6	Q961d6	drosophila	941	111.5	5.8	541	2	Q95XJ7	Q95xj7	caenorhabdi
869	113.5	5.9	1332	2	Q9BN17	Q9bn17	drosophila	942	111.5	5.8	650	1	L1B1_HUMAN	Q8nh16	h leukocyte
870	113.5	5.9	1332	2	Q9VQW7	Q9vqw7	drosophila	943	111.5	5.8	731	2	Q8SPI6	Q8spi6	macropus eu
871	113.5	5.9	1506	2	Q9V7G6	Q9v7g6	drosophila	944	111.5	5.8	782	2	Q9ESA5	Q9esa5	rattus norv
872	113.5	5.9	2051	2	Q44328	Q44328	hirudo medi	945	111.5	5.8	865	2	Q68DA2	Q68da2	homo sapien
873	113	5.9	202	2	Q7Q4106	Q7q4106	salmo sp. i	946	111.5	5.8	945	2	Q77589	Q77589	equus cabal
874	113	5.9	260	2	Q7Q411	Q7q411	anopheles g	947	111.5	5.8	949	1	MDC1_MOUSE	P60755	mus musculus
875	113	5.9	295	2	Q9QYL6	Q9qyl6	mus musculus	948	111.5	5.8	949	1	MDC1_RAT	P60756	rattus norv
876	113	5.9	308	2	Q8UV65	Q8uv65	brachydanio	949	111.5	5.8	1036	2	Q8SWF3	Q8swf3	drosophila
877	113	5.9	335	2	Q9NQ25	Q9nq25	homo sapien	950	111.5	5.8	1241	1	NPHN_HUMAN	Q60500	homo sapien
878	113	5.9	342	2	Q9IB00	Q9ib00	spherooides	951	111.5	5.8	1390	2	Q9VNI4	Q9vni4	drosophila
879	113	5.9	350	2	Q9VFU7	Q9vfu7	drosophila	952	111.5	5.8	1788	2	Q9IAJ0	Q9iaj0	xenopus lae
880	113	5.9	364	1	CD33_HUMAN	P20138	homo sapien	953	111.5	5.8	1880	2	O18465	O18465	hirudo medi
881	113	5.9	474	2	P79355	P79355	felis silve	954	111.5	5.8	1889	2	Q7Q0X2	Q7q0x2	anopheles g
882	113	5.9	526	1	CEA1_HUMAN	P13688	homo sapien	955	111.5	5.8	3262	2	Q9EQJ5	Q9eqj5	mus musculus
883	113	5.9	842	1	UNSA_HUMAN	Q6zn44	homo sapien	956	111	5.8	248	1	MYP0_RAT	P08907	rattus norv
884	113	5.9	868	1	MUSK_MOUSE	Q61006	mus musculus	957	111	5.8	290	2	Q7MSD4	Q7msd4	avian adeno
885	113	5.9	1363	1	MUSK_MOUSE	P35917	mus musculus	958	111	5.8	300	2	Q8CJ63	Q8cj63	mus musculus
886	113	5.9	1898	2	Q9EQ17	Q9eq17	mus musculus	959	111	5.8	337	2	Q6SJ07	Q6sj07	mus musculus
887	112.5	5.9	275	2	Q8AVV1	Q8avv1	xenopus lae	960	111	5.8	358	2	Q22780	Q22780	caenorhabdi
888	112.5	5.9	291	2	Q858Q7	Q858q7	homo sapien	961	111	5.8	445	2	Q8K3T6	Q8k3t6	mus musculus
889	112.5	5.9	321	2	Q9HCN7	Q9hcn7	homo sapien	962	111	5.8	451	2	Q8VD31	Q8vd31	mus musculus
890	112.5	5.9	399	2	Q9N772	Q9n772	homo sapien	963	111	5.8	641	2	Q86SD2	Q86sd2	ciona intes
891	112.5	5.9	410	2	Q6R3L9	Q6r3l9	bombyx mand	964	111	5.8	702	2	Q69ZY8	Q69zy8	mus musculus
892	112.5	5.9	410	2	Q6R3M0	Q6r3m0	bombyx mori	965	111	5.8	789	2	Q7PMB2	Q7pmb2	anopheles g
893	112.5	5.9	410	2	Q6R3M2	Q6r3m2	bombyx mori	966	111	5.8	873	1	FAS2_DROME	P34082	drosophila
894	112.5	5.9	430	2	Q7QGS8	Q7qgs8	anopheles g	967	111	5.8	980	2	Q917J1	Q917j1	drosophila
895	112.5	5.9	461	2	Q6C2X8	Q6c2x8	yarrowia li	968	111	5.8	1437	2	Q44329	Q44329	hirudo medi
896	112.5	5.9	567	2	Q96KV6	Q96kv6	homo sapien	969	111	5.8	2029	2	Q9VIS8	Q9vis8	drosophila
897	112.5	5.9	602	2	Q86YJ9	Q86yj9	homo sapien	970	110.5	5.8	277	2	Q8C6H8	Q8c6h8	mus musculus
898	112.5	5.9	650	2	Q8NA84	Q8na84	homo sapien	971	110.5	5.8	307	2	Q94431	Q94431	ciona intes
899	112.5	5.9	662	2	Q8MJZ6	Q8miz6	pan troglod	972	110.5	5.8	320	2	Q8IWO0	Q8iwo0	homo sapien
900	112.5	5.9	793	2	Q70246	Q70246	mus musculus	973	110.5	5.8	356	2	Q8AXL7	Q8axl7	oncorhynch
901	112.5	5.9	813	2	Q8BQC3	Q8bqc3	mus musculus	974	110.5	5.8	504	2	Q6NNA1	Q6nnal	drosophila
902	112.5	5.9	824	2	Q90749	Q90749	gallus gall	975	110.5	5.8	508	2	Q9VGD2	Q9vgd2	drosophila
903	112.5	5.9	1032	2	Q9AXZ4	Q9axz4	brachydanio	976	110.5	5.8	551	1	SIL5_HUMAN	O15389	homo sapien
904	112.5	5.9	1065	1	L1G2_HUMAN	Q94898	homo sapien	977	110.5	5.8	664	2	Q9VGD3	Q9vgd3	drosophila
905	112.5	5.9	1561	2	Q224D2	Q224d2	mus musculus	978	110.5	5.8	868	1	MUSK_RAT	Q62838	rattus norv
906	112.5	5.9	1940	2	Q6PDN3	Q6pdn3	mus musculus	979	110.5	5.8	907	2	Q98850	Q98850	carassius a
907	112.5	5.9	1950	2	Q80YN8	Q80yn8	mus musculus	980	110.5	5.8	1023	2	Q9ULI7	Q9uli7	homo sapien

981	110.5	5.8	1185	2	Q7PRK4	Q7prk4 anopheles g	1054	109	5.7	2169	2	Q8AV58	Q8av58 gallus gall
982	110.5	5.8	1248	2	Q9XT41	Q9xt41 cercopithec	1055	108.5	5.7	215	1	CIB3_HUMAN	Q9ny72 homo sapien
983	110.5	5.8	1898	2	Q84604	Q84604 r protein-t	1056	108.5	5.7	277	2	Q6IEE8	Q6iee8 rattus norv
984	110	5.8	198	2	Q6NVX7	Q6nvx7 homo sapien	1057	108.5	5.7	283	2	Q7QGT4	Q7qgt4 anopheles g
985	110	5.8	238	2	Q20339	Q20339 caenorhabdi	1058	108.5	5.7	285	1	FCG2_RAT	Q63203 rattus norv
986	110	5.8	270	1	BASI_RABIT	Q28740 oryctolagus	1059	108.5	5.7	306	2	Q9QYL4	Q9qyl4 mus musculus
987	110	5.8	282	2	Q7TPU2	Q7tpu2 mus musculus	1060	108.5	5.7	313	2	Q65801	Q65801 ceratopteri
988	110	5.8	296	1	FCG2_BOVIN	Q28110 bos taurus	1061	108.5	5.7	325	1	NCT1_RAT	Q920h5 rattus norv
989	110	5.8	301	2	Q96K94	Q96k94 homo sapien	1062	108.5	5.7	357	2	Q8RL12	Q8rl12 mus musculus
990	110	5.8	324	2	Q7TMD2	Q7tmd2 mus musculus	1063	108.5	5.7	394	2	Q6TGR9	Q6tgr9 oryctolagus
991	110	5.8	330	1	FCG2_MOUSE	P08101 mus musculus	1064	108.5	5.7	462	2	Q7RTW1	Q7rtw1 homo sapien
992	110	5.8	343	2	Q84Y0	Q84y0 mus musculus	1065	108.5	5.7	483	2	Q7SX76	Q7sx76 brachydanio
993	110	5.8	422	1	K3L1_RAT	P83556 rattus norv	1066	108.5	5.7	537	2	Q9MZU5	Q9mzu5 sus scrofa
994	110	5.8	428	2	Q96PJ6	Q96pj6 homo sapien	1067	108.5	5.7	552	2	Q7QFF0	Q7qff0 anopheles g
995	110	5.8	429	2	Q96LA6	Q96la6 homo sapien	1068	108.5	5.7	570	2	Q6GLY1	Q6gly1 xenopus lae
996	110	5.8	459	2	Q9JHL6	Q9jhl6 rattus norv	1069	108.5	5.7	639	1	NRG1_HUMAN	Q02297 h pro-neure
997	110	5.8	467	2	Q91VT9	Q91vt9 mus musculus	1070	108.5	5.7	640	2	Q7RTV8	Q7rtv8 homo sapien
998	110	5.8	525	2	Q6XJ01	Q6xjq1 rattus norv	1071	108.5	5.7	646	1	MU18_HUMAN	P43121 homo sapien
999	110	5.8	536	2	Q8GV82	Q8gv82 drosophila	1072	108.5	5.7	653	1	RIPA_HUMAN	Q9bxf6 homo sapien
1000	110	5.8	635	2	P91092	P91092 caenorhabdi	1073	108.5	5.7	764	1	P1GR_HUMAN	P01833 homo sapien
1001	110	5.8	643	2	Q95Q79	Q95q79 caenorhabdi	1074	108.5	5.7	974	2	Q63702	Q63702 rattus ratt
1002	110	5.8	752	2	Q9XYS4	Q9xys4 hydra atten	1075	108.5	5.7	2016	2	Q8MKM6	Q8mkm6 drosophila
1003	110	5.8	761	2	Q9NL40	Q9nl40 asterina pe	1076	108.5	5.7	2016	2	Q8MKM7	Q8mkm7 drosophila
1004	110	5.8	788	2	Q9CYK3	Q9cyk3 mus musculus	1077	108.5	5.7	2016	2	Q9NBA1	Q9nba1 drosophila
1005	110	5.8	799	1	ITEN_DROME	Q27591 drosophila	1078	108.5	5.7	2019	2	Q8MKM8	Q8mkm8 drosophila
1006	110	5.8	804	2	Q800Z1	Q800z1 brachydanio	1079	108.5	5.7	2222	2	Q97394	Q97394 drosophila
1007	110	5.8	812	2	Q8N612	Q8n612 homo sapien	1080	108.5	5.7	2230	2	Q86BQ7	Q86bq7 drosophila
1008	110	5.8	833	2	Q80TG9	Q80tg9 mus musculus	1081	108.5	5.7	2935	2	Q7Z1Y4	Q7z1y4 drosophila
1009	110	5.8	886	2	Q9VM64	Q9vm64 drosophila	1082	108.5	5.7	2946	2	Q9NW53	Q9nw53 drosophila
1010	110	5.8	924	1	ICA5_HUMAN	Q9umf0 homo sapien	1083	108	5.7	143	2	Q9NU62	Q9nu62 homo sapien
1011	110	5.8	924	2	Q8TAM9	Q8tam9 homo sapien	1084	108	5.7	248	1	MYPO_HUMAN	P25189 homo sapien
1012	110	5.8	987	2	Q7YZM8	Q7yzm8 caenorhabdi	1085	108	5.7	248	2	Q6P0H1	Q6p0h1 brachydanio
1013	110	5.8	1005	2	P79921	P79921 xenopus lae	1086	108	5.7	301	2	Q8TDQ0	Q8tdq0 homo sapien
1014	110	5.8	1040	1	EG15_CAEL	Q10656 caenorhabdi	1087	108	5.7	333	2	Q86WB8	Q86wb8 homo sapien
1015	110	5.8	1051	2	Q7JL68	Q7jl68 caenorhabdi	1088	108	5.7	333	2	Q90Z41	Q90z41 gallus gall
1016	110	5.8	1096	2	Q8MQ14	Q8mq14 caenorhabdi	1089	108	5.7	343	2	Q8BYS4	Q8bys4 mus musculus
1017	110	5.8	1252	2	Q9EQS9	Q9eqs9 mus musculus	1090	108	5.7	406	2	Q6R3N3	Q6r3n3 sus scrofa
1018	110	5.8	1271	2	Q6U714	Q6u714 brachydanio	1091	108	5.7	443	2	Q8N2F4	Q8n2f4 homo sapien
1019	110	5.8	1383	2	Q7Q840	Q7q840 anopheles g	1092	108	5.7	447	2	Q6R3N4	Q6r3n4 sus scrofa
1020	110	5.8	1876	1	VIT2_PERAM	Q9bpo0 peripianeta	1093	108	5.7	448	2	Q9JHL7	Q9jhl7 rattus norv
1021	110	5.8	1896	2	Q9IAJ1	Q9iaj1 xenopus lae	1094	108	5.7	457	2	Q6GYR3	Q6gyr3 sus scrofa
1022	110	5.8	2693	2	Q8ISF3	Q8isf3 caenorhabdi	1095	108	5.7	483	1	L1A2_HUMAN	Q8ni49 homo sapien
1023	110	5.8	2708	2	Q8ISP4	Q8isf4 caenorhabdi	1096	108	5.7	527	2	Q6ZTR2	Q6ztr2 homo sapien
1024	110	5.8	18519	2	Q8ISF6	Q8isf6 caenorhabdi	1097	108	5.7	588	1	C166_CHICK	P42292 gallus gall
1025	110	5.8	18534	2	Q8ISF7	Q8isf7 caenorhabdi	1098	108	5.7	626	1	MAG_MOUSE	P20917 mus musculus
1026	109.5	5.7	333	2	Q8UV75	Q8uv75 brachydanio	1099	108	5.7	626	2	Q6DCH3	Q6dch3 xenopus lae
1027	109.5	5.7	336	2	Q8UV73	Q8uv73 brachydanio	1100	108	5.7	646	2	Q6PHR3	Q6phr3 homo sapien
1028	109.5	5.7	341	2	Q61353	Q61353 mus musculus	1101	108	5.7	757	2	Q7QCU0	Q7qcu0 anopheles g
1029	109.5	5.7	442	2	Q9BY67	Q9by67 homo sapien	1102	108	5.7	812	1	FGR1_XENLA	P22182 xenopus lae
1030	109.5	5.7	523	2	Q80ZE2	Q80ze2 mus musculus	1103	108	5.7	997	2	Q7PX30	Q7px30 anopheles g
1031	109.5	5.7	527	1	E4L8_MOUSE	Q9jmc8 mus musculus	1104	108	5.7	1035	2	Q9NEG1	Q9neg1 drosophila
1032	109.5	5.7	686	1	IFL2_MOUSE	Q9ers6 mus musculus	1105	108	5.7	1459	1	YF1M_CAEL	Q21874 caenorhabdi
1033	109.5	5.7	729	1	FGR1_DROME	Q07407 drosophila	1106	108	5.7	1555	2	Q7PPH8	Q7pph8 anopheles g
1034	109.5	5.7	741	2	Q6RCF4	Q6rcf4 vibriophaga	1107	108	5.7	1608	2	Q7PR41	Q7pr41 anopheles g
1035	109.5	5.7	1014	2	Q8NFA6	Q8nfa6 homo sapien	1108	108	5.7	1887	2	Q9QW67	Q9qw67 rattus sp.
1036	109.5	5.7	1026	2	Q6ZQD0	Q6zqd0 mus musculus	1109	108	5.7	2389	2	Q6BE05	Q6beq6 caenorhabdi
1037	109.5	5.7	1242	1	NPHN_MOUSE	Q9qzs7 mus musculus	1110	107.5	5.6	283	2	Q8PG31	Q8pg31 brachydanio
1038	109	5.7	203	2	Q8JFG6	Q8jfg6 brachydanio	1111	107.5	5.6	309	1	CD86_MOUSE	P42082 mus musculus
1039	109	5.7	240	2	Q6TYZ5	Q6tyz5 canis fami1	1112	107.5	5.6	314	2	Q61238	Q61238 mus musculus
1040	109	5.7	248	2	Q6WEB5	Q6web5 equus cabal	1113	107.5	5.6	323	2	Q9ESA2	Q9esa2 rattus norv
1041	109	5.7	270	2	Q6AYT8	Q6ayt8 rattus norv	1114	107.5	5.6	329	2	Q9IAY6	Q9iay6 spherooides
1042	109	5.7	272	2	Q9UIB7	Q9uib7 homo sapien	1115	107.5	5.6	356	2	Q64381	Q64381 mus musculus
1043	109	5.7	280	2	Q95660	Q95660 homo sapien	1116	107.5	5.6	370	2	Q800Y8	Q800y8 brachydanio
1044	109	5.7	283	2	Q7TSP5	Q7tsp5 mus musculus	1117	107.5	5.6	454	2	Q91W54	Q91w54 mus musculus
1045	109	5.7	333	2	Q9IB04	Q9ib04 spherooides	1118	107.5	5.6	455	2	Q71QE2	Q71qe2 tursiops tr
1046	109	5.7	407	2	Q9Y412	Q9y412 homo sapien	1119	107.5	5.6	467	1	SIL7_HUMAN	Q9y286 homo sapien
1047	109	5.7	500	2	Q9W260	Q9w260 drosophila	1120	107.5	5.6	489	1	L1A1_HUMAN	Q75019 homo sapien
1048	109	5.7	500	2	Q9XZB7	Q9xzb7 drosophila	1121	107.5	5.6	538	2	Q8L7B6	Q8l7b6 arabidopsis
1049	109	5.7	626	1	MAG_RAT	P07722 rattus norv	1122	107.5	5.6	622	2	Q9ESS5	Q9ess5 mus musculus
1050	109	5.7	645	2	Q7RTW4	Q7rtw4 homo sapien	1123	107.5	5.6	622	2	Q9UKB2	Q9ukb2 mus musculus
1051	109	5.7	869	1	MUSK_HUMAN	O15146 homo sapien	1124	107.5	5.6	622	2	Q9RO69	Q9ro69 mus musculus
1052	109	5.7	1264	2	O14631	O14631 homo sapien	1125	107.5	5.6	645	2	O22701	O22701 arabidopsis
1053	109	5.7	1298	1	VGR3_HUMAN	P35916 homo sapien	1126	107.5	5.6	650	2	Q99K86	Q99k86 mus musculus

1127	107.5	5.6	652	2	Q84MA9	Q84ma9 arabidopsis	1200	105.5	5.5	301	2	Q7Q864	Q7q864 anopheles g
1128	107.5	5.6	697	2	Q7PMJ7	Q7pmj7 anopheles g	1201	105.5	5.5	307	2	Q7PCU3	Q7pcu3 anopheles g
1129	107.5	5.6	697	2	Q8K4V6	Q8k4v6 mus musculus	1202	105.5	5.5	320	2	Q9IAZ9	Q9iaz9 spherooides
1130	107.5	5.6	814	2	Q91897	Q91897 xenopus lae	1203	105.5	5.5	324	2	Q8NBY8	Q8ncb7 homo sapien
1131	107.5	5.6	1029	2	Q9W3D9	Q9w3d9 drosophila	1204	105.5	5.5	326	2	Q8NC17	Q8nc17 homo sapien
1132	107.5	5.6	1256	2	Q9JIX1	Q9jix1 mus musculus	1205	105.5	5.5	330	2	Q90Z42	Q90z42 gallus gall
1133	107.5	5.6	1304	1	NRCA_HUMAN	NRCA_HUMAN	1206	105.5	5.5	403	2	Q6NZV3	Q6nzv3 brachydanio
1134	107.5	5.6	1369	1	NRAS_CHICK	NRAS_CHICK	1207	105.5	5.5	433	2	Q00002	Q00002 altermaria
1135	107	5.6	202	2	Q9ERP6	Q9erp6 rattus norv	1208	105.5	5.5	441	2	Q9DDC4	Q9ddc4 oncorhynch
1136	107	5.6	320	2	Q7Q0P8	Q7q0p8 anopheles g	1209	105.5	5.5	455	2	Q9XS78	Q9xs78 delphinapte
1137	107	5.6	330	2	Q63241	Q63241 rattus norv	1210	105.5	5.5	457	1	CD4_RAT	P05540 rattus norv
1138	107	5.6	335	2	Q75237	Q75237 homo sapien	1211	105.5	5.5	474	2	Q8K178	Q8k178 mus musculus
1139	107	5.6	353	2	Q63242	Q63242 rattus norv	1212	105.5	5.5	645	2	Q6DR98	Q6dr98 mus musculus
1140	107	5.6	446	2	Q63237	Q63237 rattus norv	1213	105.5	5.5	694	2	Q8SWT7	Q8swt7 drosophila
1141	107	5.6	743	2	Q6P1M7	Q6p1m7 homo sapien	1214	105.5	5.5	740	2	Q9UPF2	Q9upf2 homo sapien
1142	107	5.6	771	2	Q8N116	Q8n116 homo sapien	1215	105.5	5.5	843	1	CYP1_BRUMA	Q27450 brugia mala
1143	107	5.6	1011	2	Q24273	Q24273 drosophila	1216	105.5	5.5	997	2	Q44087	Q44087 caenorhabdi
1144	107	5.6	1164	2	Q66MN5	Q66mn5 drosophila	1217	105.5	5.5	999	1	MERK_HUMAN	Q12866 homo sapien
1145	107	5.6	1265	2	Q9P274	Q9p274 homo sapien	1218	105.5	5.5	1345	2	Q8VCD0	Q8vcd0 mus musculus
1146	107	5.6	1817	2	Q7SZF6	Q7szf6 xenopus lae	1219	105.5	5.5	1367	1	VGR2_MOUSE	P35918 mus musculus
1147	107	5.6	1897	1	PTPF_HUMAN	PTPF_HUMAN	1220	105.5	5.5	1894	2	Q64487	Q64487 mus musculus
1148	107	5.6	1898	2	Q86WS0	Q86ws0 homo sapien	1221	105.5	5.5	4203	2	Q965G2	Q965g2 caenorhabdi
1149	107	5.6	5604	2	Q8WZ53	Q8wz53 homo sapien	1222	105.5	5.5	4219	2	Q9NL87	Q9nl87 caenorhabdi
1150	107	5.6	26926	2	Q10466	Q10466 homo sapien	1223	105.5	5.5	4447	2	Q8MXD8	Q8mxd8 caenorhabdi
1151	107	5.6	26926	2	Q8WZB3	Q8wzb3 homo sapien	1224	105.5	5.5	4488	2	Q9TXK2	Q9txk2 caenorhabdi
1152	106.5	5.6	163	2	Q8K1H8	Q8k1h8 mus musculus	1225	105	5.5	219	1	MYP0_BOVIN	P10522 bos taurus
1153	106.5	5.6	251	2	Q14902	Q14902 homo sapien	1226	105	5.5	229	2	Q9TT71	Q9tt71 sus scrofa
1154	106.5	5.6	258	2	Q12811	Q12811 homo sapien	1227	105	5.5	230	2	Q9N2I3	Q9n2i3 sus scrofa
1155	106.5	5.6	337	2	Q9IAZ4	Q9iaz4 spherooides	1228	105	5.5	278	2	Q6UM59	Q6um59 homo sapien
1156	106.5	5.6	349	1	CEA8_HUMAN	P31997 homo sapien	1229	105	5.5	283	2	Q7TPH5	Q7tpH5 mus musculus
1157	106.5	5.6	351	2	Q15225	Q15225 homo sapien	1230	105	5.5	329	1	CD86_HUMAN	P42081 homo sapien
1158	106.5	5.6	364	2	Q76LL0	Q76l10 coturnix co	1231	105	5.5	330	2	P97269	P97269 cavia porce
1159	106.5	5.6	416	2	Q9KGK6	Q9kgk6 bacillus ha	1232	105	5.5	336	2	Q90Z89	Q90z89 brachydanio
1160	106.5	5.6	440	2	Q8MK39	Q8mk39 macaca mula	1233	105	5.5	360	2	Q8N732	Q8n732 homo sapien
1161	106.5	5.6	456	2	Q8R5M8	Q8r5m8 mus musculus	1234	105	5.5	426	2	Q6LEU7	Q6leu7 homo sapien
1162	106.5	5.6	475	2	Q8NCW2	Q8ncw2 homo sapien	1235	105	5.5	544	1	ICA3_BOVIN	Q28125 bos taurus
1163	106.5	5.6	475	2	Q8NCW3	Q8ncw3 homo sapien	1236	105	5.5	562	2	Q9LXU9	Q9lXu9 arabidopsis
1164	106.5	5.6	724	2	Q9MYN0	Q9myrn0 bos taurus	1237	105	5.5	672	2	Q7RTW3	Q7rtw3 homo sapien
1165	106.5	5.6	764	2	Q8IZY7	Q8izy7 homo sapien	1238	105	5.5	676	2	Q6ZPB7	Q6zpb7 oryza sativ
1166	106.5	5.6	806	2	Q90Z00	Q90z00 brachydanio	1239	105	5.5	688	2	Q80ZE3	Q80ze3 mus musculus
1167	106.5	5.6	824	2	Q91286	Q91286 pleurodeles	1240	105	5.5	789	2	Q9BE71	Q9be71 macaca faec
1168	106.5	5.6	972	2	Q76110	Q76i10 callithrix	1241	105	5.5	1182	2	Q9V7C1	Q9v7c1 magnaporthe
1169	106.5	5.6	975	1	KIT_CANFA	Q97799 canis famil	1242	105	5.5	1709	1	SN_HUMAN	Q9b222 homo sapien
1170	106.5	5.6	975	2	Q7YRV7	Q7yrv7 canis famil	1243	104.5	5.5	215	1	CIB3_RAT	Q9Jk00 rattus norv
1171	106.5	5.6	977	1	KIT_BOVIN	P43481 bos taurus	1244	104.5	5.5	241	2	Q07112	Q07112 bos taurus
1172	106.5	5.6	978	2	Q63116	Q63116 rattus norv	1245	104.5	5.5	283	2	Q6NZV7	Q6nzv7 brachydanio
1173	106.5	5.6	1196	2	Q96VN4	Q96vn4 coccidioid	1246	104.5	5.5	334	2	Q819N0	Q819n0 branciocto
1174	106.5	5.6	1250	2	Q8TDY8	Q8tdy8 homo sapien	1247	104.5	5.5	339	2	Q9UIE2	Q9uif2 homo sapien
1175	106.5	5.6	1331	2	Q7Q623	Q7q623 anopheles g	1248	104.5	5.5	430	2	Q76LJ8	Q76lj8 coturnix co
1176	106	5.6	187	2	Q7KAB2	Q7ka82 drosophila	1249	104.5	5.5	460	2	Q8MJ24	Q8mj24 pan troglod
1177	106	5.6	292	2	Q02758	Q02758 felis silve	1250	104.5	5.5	542	2	Q8NH5	Q8nh5 homo sapien
1178	106	5.6	292	2	Q9GMZ8	Q9gmz8 felis silve	1251	104.5	5.5	602	2	Q7TMW0	Q7tmw0 mus musculus
1179	106	5.6	296	2	Q46405	Q46405 bos taurus	1252	104.5	5.5	685	1	IPL2_HUMAN	Q9np60 h x-linked
1180	106	5.6	336	2	Q80VG4	Q80vg4 mus musculus	1253	104.5	5.5	775	2	Q6PF50	Q6pf50 xenopus lae
1181	106	5.6	336	2	Q9D6E7	Q9d6e7 mus musculus	1254	104.5	5.5	810	2	Q9PS96	Q9ps96 xenopus lae
1182	106	5.6	337	2	Q8UV29	Q8uv29 brachydanio	1255	104.5	5.5	813	2	Q80TK8	Q80tk8 mus musculus
1183	106	5.6	340	2	Q9W3N2	Q9w3n2 drosophila	1256	104.5	5.5	955	1	MDG1_HUMAN	Q8nfp4 homo sapien
1184	106	5.6	341	2	Q61354	Q61354 mus musculus	1257	104.5	5.5	978	1	KIT_CAPHI	Q28317 capra hircu
1185	106	5.6	361	2	Q68ML2	Q6bwl2 debaryomyce	1258	104.5	5.5	978	2	Q9XS93	Q9xs93 canis famil
1186	106	5.6	466	2	Q6UXB8	Q6uxb8 homo sapien	1259	104.5	5.5	979	2	Q8WN23	Q8wn23 canis famil
1187	106	5.6	554	2	Q9W4R3	Q9w4r3 drosophila	1260	104.5	5.5	986	2	Q8UVR9	Q8uvr9 fugu rubrip
1188	106	5.6	558	1	C166_CARAU	Q90304 carassius a	1261	104.5	5.5	1184	2	Q8C1B1	Q8c1b1 mus musculus
1189	106	5.6	558	2	Q6PDB1	Q6pdb1 homo sapien	1262	104.5	5.5	1284	1	NRCA_CHICK	P35331 gallus gall
1190	106	5.6	637	2	Q6NSGO	Q6nsg0 homo sapien	1263	104.5	5.5	1443	1	NEO1_CHICK	Q90610 gallus gall
1191	106	5.6	686	1	SILB_HUMAN	Q9er16 homo sapien	1264	104.5	5.5	1685	2	Q7RZ66	Q7rze6 neurospora
1192	106	5.6	719	1	LRF5_MOUSE	Q8bxa0 mus musculus	1265	104.5	5.5	7105	2	Q7PXM9	Q7pxw9 anopheles g
1193	106	5.6	719	2	Q84VG3	Q84vg3 oryza sativ	1266	104	5.5	133	2	Q860H6	Q860h6 gallus gall
1194	106	5.6	841	2	O54999	O54999 mus musculus	1267	104	5.5	242	2	Q46604	Q46604 sus scrofa
1195	106	5.6	2558	1	Q6NR91	Q6nr91 drosophila	1268	104	5.5	268	2	Q46603	Q46603 sus scrofa
1196	105.5	5.5	211	2	Q8BK18	Q8bk18 mus musculus	1269	104	5.5	282	2	Q96BF3	Q96bf3 homo sapien
1197	105.5	5.5	215	1	CIB3_MOUSE	Q8bhk2 mus musculus	1270	104	5.5	316	2	Q8WPB3	Q8wpb3 drosophila
1198	105.5	5.5	268	2	Q9ZQ33	Q9zq33 mus musculus	1271	104	5.5	337	2	Q8UB51	Q8ub51 brachydanio
1199	105.5	5.5	287	2	Q9UD97	Q9ud97 homo sapien	1272	104	5.5	357	2	O18872	O18872 sus scrofa

1273	104	5.5	370	2	Q6MZQ3	Q6mzq3 homo sapien	1346	103	5.4	1485	1	TOP2_SCHPO	P08096 schizosacch
1274	104	5.5	426	1	PSG9_HUMAN	Q00887 homo sapien	1347	103	5.4	16223	2	Q81R22	Q81r22 drosophila
1275	104	5.5	431	2	Q8H8V1	Q9h8v1 homo sapien	1348	102.5	5.4	241	2	Q6PK61	Q6pk61 homo sapien
1276	104	5.5	439	2	Q6GTU4	Q6gtu4 homo sapien	1349	102.5	5.4	281	2	Q8VIM0	Q8vim0 mus musculus
1277	104	5.5	463	1	SIL9_HUMAN	Q9y336 homo sapien	1350	102.5	5.4	302	1	ICOL_HUMAN	O75144 homo sapien
1278	104	5.5	499	2	Q7SFE6	Q7sfe6 neurospora	1351	102.5	5.4	310	2	Q8SPW4	Q8spw4 macaca fasc
1279	104	5.5	538	1	PVR2_HUMAN	Q92692 homo sapien	1352	102.5	5.4	318	2	Q90Z81	Q90z81 brachydanio
1280	104	5.5	646	2	Q958I2	Q95812 homo sapien	1353	102.5	5.4	324	2	Q8UV37	Q8uv37 brachydanio
1281	104	5.5	716	2	Q8IYV5	Q8iyy5 homo sapien	1354	102.5	5.4	325	2	O02838	O02838 sus scrofa
1282	104	5.5	716	2	Q6UXK5	Q6uxk5 homo sapien	1355	102.5	5.4	341	1	FCG2_CAVPO	Q60513 cavia porce
1283	104	5.5	718	2	Q73675	Q73675 xenopus lae	1356	102.5	5.4	429	1	EPC_RAT	P01855 rattus norv
1284	104	5.5	718	2	Q6PCK4	Q6pck4 xenopus lae	1357	102.5	5.4	521	1	L6G3_MOUSE	Q61790 mus musculus
1285	104	5.5	730	2	Q9P231	Q9p231 homo sapien	1358	102.5	5.4	570	2	Q6GMZ9	Q6gmz9 xenopus lae
1286	104	5.5	832	2	Q8ULH4	Q8ulh4 homo sapien	1359	102.5	5.4	640	1	DIM1_CABEL	Q18066 caenorhabdi
1287	104	5.5	976	2	Q8JFR5	Q8jfr5 brachydanio	1360	102.5	5.4	798	2	Q86K66	Q86k66 dictyosteli
1288	104	5.5	1003	2	Q90060	Q90060 trypanosoma	1361	102.5	5.4	885	2	Q8HYV1	Q8hyv1 sus scrofa
1289	104	5.5	1134	2	Q71B05	Q71b05 brachydanio	1362	102.5	5.4	886	2	Q8HYV2	Q8hyv2 sus scrofa
1290	104	5.5	1142	2	Q18100	Q18100 caenorhabdi	1363	102.5	5.4	1151	2	Q9QVN5	Q9qvn5 rattus sp.
1291	104	5.5	1224	2	O00533	Q00533 homo sapien	1364	102.5	5.4	1155	2	Q82RF1	Q82rf1 streptomyce
1292	104	5.5	1235	2	Q7Q0S7	Q7q0s7 anopheles g	1365	102.5	5.4	1240	1	NFAS_MOUSE	Q810u3 mus musculus
1293	104	5.5	1250	2	Q88971	Q88971 mus musculus	1366	102.5	5.4	1240	1	NFAS_RAT	P97685 rattus norv
1294	104	5.5	1251	2	Q6ZQ54	Q6zq54 mus musculus	1367	102.5	5.4	1735	2	Q7Q9I6	Q7q9i6 anopheles g
1295	104	5.5	1277	1	CAML_FUGRU	Q98902 fugu rubrip	1368	102.5	5.4	1876	2	O02024	O02024 riptortus c
1296	104	5.5	1447	1	DCC_MOUSE	P70211 mus musculus	1369	102.5	5.4	6839	2	Q23550	Q23550 caenorhabdi
1297	104	5.5	1779	2	Q74BG8	Q74bg8 geobacter s	1370	102.5	5.4	7158	2	Q23551	Q23551 caenorhabdi
1298	104	5.5	1912	1	PTPD_HUMAN	P23468 homo sapien	1371	102	5.3	192	2	Q9ERP7	Q9erp7 rattus norv
1299	103.5	5.4	211	2	Q7RTW5	Q7rtw5 homo sapien	1372	102	5.3	295	2	Q9ERF5	Q9erf5 mesocricetu
1300	103.5	5.4	239	2	O44730	Q44730 caenorhabdi	1373	102	5.3	324	2	Q9UPK9	Q9upk9 homo sapien
1301	103.5	5.4	241	2	Q7RTW0	Q7rtw0 homo sapien	1374	102	5.3	326	2	Q9UPK8	Q9upk8 homo sapien
1302	103.5	5.4	336	2	Q8UV41	Q8uv41 brachydanio	1375	102	5.3	333	2	O75238	O75238 homo sapien
1303	103.5	5.4	360	2	Q8BJ10	Q8bj10 mus musculus	1376	102	5.3	340	2	Q9IAZ6	Q9iaz6 spherooides
1304	103.5	5.4	410	2	Q7YZA7	Q7yza7 bombyx mori	1377	102	5.3	353	2	Q9BCW3	Q9bcw3 gallus gall
1305	103.5	5.4	457	2	Q8HZT8	Q8hzt8 callithrix	1378	102	5.3	437	2	Q90WL4	Q90wl4 gallus gall
1306	103.5	5.4	662	1	NRG1_RAT	P43322 r pro-neure	1379	102	5.3	442	2	Q7PT04	Q7pt04 anopheles g
1307	103.5	5.4	717	2	Q7PUQ1	Q7puq1 anopheles g	1380	102	5.3	527	2	O94040	O94040 candida alb
1308	103.5	5.4	1007	1	ROB4_HUMAN	Q8wz75 homo sapien	1381	102	5.3	571	2	Q8QFN4	Q8qfn4 salmo salar
1309	103.5	5.4	1232	2	Q90284	Q90284 carassius a	1382	102	5.3	595	1	SILL_HUMAN	Q96pq1 homo sapien
1310	103.5	5.4	1256	2	Q925S5	Q925s5 mus musculus	1383	102	5.3	638	2	Q7Q766	Q7q766 anopheles g
1311	103.5	5.4	1256	2	Q92TS9	Q9et59 mus musculus	1384	102	5.3	670	2	Q7ZZ47	Q7zz47 brachydanio
1312	103.5	5.4	1375	2	Q8ML47	Q8ml47 drosophila	1385	102	5.3	709	2	Q8IXC7	Q8ixc7 homo sapien
1313	103.5	5.4	1375	2	Q94537	Q94537 drosophila	1386	102	5.3	718	2	Q6P627	Q6p627 xenopus lae
1314	103.5	5.4	1427	2	Q15662	Q91562 xenopus lae	1387	102	5.3	808	2	Q7FVZ3	Q7pvr3 anopheles g
1315	103.5	5.4	1447	1	DCC_HUMAN	P43146 homo sapien	1388	102	5.3	814	2	Q81VU1	Q81vu1 homo sapien
1316	103.5	5.4	1526	2	Q94538	Q94538 drosophila	1389	102	5.3	848	2	O25198	O25198 hydra atten
1317	103.5	5.4	1526	2	Q9V6D5	Q9v6d5 drosophila	1390	102	5.3	975	2	P79750	P79750 fugu rubrip
1318	103.5	5.4	3094	2	Q695L1	Q695l1 homo sapien	1391	102	5.3	1044	2	Q961W3	Q96iw3 homo sapien
1319	103	5.4	295	2	Q9GL75	Q9gl75 bos taurus	1392	102	5.3	1089	2	Q19927	Q19927 caenorhabdi
1320	103	5.4	296	2	Q8WMZ2	Q8wmz2 sus scrofa	1393	102	5.3	1173	2	Q6NR54	Q6nr54 drosophila
1321	103	5.4	310	2	Q7QK35	Q7qk35 anopheles g	1394	102	5.3	1298	2	Q86W08	Q8vw08 homo sapien
1322	103	5.4	316	2	Q7Q0P9	Q7q0p9 anopheles g	1395	102	5.3	1301	2	Q9VZ81	Q9vz81 drosophila
1323	103	5.4	331	2	Q63239	Q63239 rattus norv	1396	102	5.3	1363	2	Q86W07	Q8vw07 homo sapien
1324	103	5.4	357	2	Q63238	Q63238 rattus norv	1397	102	5.3	1377	2	Q9VJ42	Q9vj42 drosophila
1325	103	5.4	446	2	Q93236	Q63236 rattus norv	1398	102	5.3	4039	2	Q7ZZ46	Q7zz46 brachydanio
1326	103	5.4	484	2	Q99JQ8	Q99jq8 mus musculus	1399	101.5	5.3	226	1	C79A_HUMAN	P11912 homo sapien
1327	103	5.4	504	2	Q8MIS3	Q8mis3 didelphis m	1400	101.5	5.3	240	2	Q13178	Q13178 homo sapien
1328	103	5.4	538	2	Q9QY07	Q9qyg7 mus musculus	1401	101.5	5.3	240	2	Q7PRJ5	Q7prj5 anopheles g
1329	103	5.4	547	2	Q6MG93	Q6mg93 rattus norv	1402	101.5	5.3	303	2	Q7T114	Q7t114 brachydanio
1330	103	5.4	569	1	TACT_HUMAN	P40200 homo sapien	1403	101.5	5.3	310	2	Q6MG95	Q6mg95 rattus norv
1331	103	5.4	601	1	Q99M67	Q99m67 mus musculus	1404	101.5	5.3	318	2	Q90Z82	Q90z82 brachydanio
1332	103	5.4	624	2	Q9ESS6	Q9ess6 rattus norv	1405	101.5	5.3	332	2	Q9GMZ7	Q9gmz7 felis silve
1333	103	5.4	645	2	Q8MJZ5	Q8mjz5 pan troglod	1406	101.5	5.3	402	2	Q15227	Q15227 homo sapien
1334	103	5.4	678	2	Q6PGN8	Q6pgn8 homo sapien	1407	101.5	5.3	423	2	Q6CTJ9	Q6ctj9 kluyveromyc
1335	103	5.4	680	2	O55001	O55001 mus musculus	1408	101.5	5.3	457	2	Q61396	Q61396 mus musculus
1336	103	5.4	739	1	VCA1_RAT	P29534 rattus norv	1409	101.5	5.3	461	2	O35947	O35947 mesocricetu
1337	103	5.4	898	1	UNSA_MOUSE	Q8k184 mus musculus	1410	101.5	5.3	597	1	SILL_PANTR	Q95lho pan troglod
1338	103	5.4	904	2	Q6P0Q2	Q6p0q2 homo sapien	1411	101.5	5.3	602	2	Q8C906	Q8c9u6 mus musculus
1339	103	5.4	960	2	Q7PV74	Q7pv74 anopheles g	1412	101.5	5.3	873	2	Q98949	Q98949 gallus gall
1340	103	5.4	1019	2	Q8IVR8	Q8ivr8 fugu rubrip	1413	101.5	5.3	939	2	Q9VH85	Q9vh85 drosophila
1341	103	5.4	1189	2	Q9P2J2	Q9p2j2 homo sapien	1414	101.5	5.3	948	2	Q9VME2	Q9vme2 drosophila
1342	103	5.4	1240	1	NFAS_HUMAN	Q94856 homo sapien	1415	101.5	5.3	1166	2	Q9QVNA	Q9qvn2 rattus sp.
1343	103	5.4	1259	1	CAML_RAT	Q05695 rattus norv	1416	101.5	5.3	1249	2	Q7IMZ9	Q7imz9 rattus norv
1344	103	5.4	1280	2	Q9EPX2	Q9epx2 mus musculus	1417	101.5	5.3	1259	2	Q6PGJ3	Q6pgj3 mus musculus
1345	103	5.4	1365	2	Q9UPS4	Q9ups4 homo sapien	1418	101.5	5.3	6048	2	Q7JN85	Q7jn85 caenorhabdi

1419	101	5.3	215	1	EVAL MOUSE	070255	mus musculus	Q70255	mus musculus	1492	100.5	5.3	1363	2	Q7Z3G9	Q7z3g9 homo sapien
1420	101	5.3	215	2	Q91W14	Q91w14	mus musculus	Q91w14	mus musculus	1493	100.5	5.3	1391	2	Q8GQP2	Q8gqp2 haemophilus
1421	101	5.3	265	2	Q7PUU3	Q7puu3	anopheles g	Q7puu3	anopheles g	1494	100.5	5.3	1401	2	Q6AWC0	Q6awc0 homo sapien
1422	101	5.3	305	2	Q75308	Q75308	homo sapien	Q75308	homo sapien	1495	100.5	5.3	1401	2	Q6AWC1	Q6awc1 homo sapien
1423	101	5.3	316	2	Q8WP58	Q8wp58	drosoophila	Q8wp58	drosoophila	1496	100.5	5.3	1461	2	Q8T9F6	Q8t9f6 drosoophila
1424	101	5.3	316	2	Q8WP94	Q8wp94	drosoophila	Q8wp94	drosoophila	1497	100.5	5.3	1474	2	Q8T4M0	Q8t4m0 drosoophila
1425	101	5.3	333	1	Q7KX22	Q7kx22	drosoophila	Q7kx22	drosoophila	1498	100.5	5.3	1503	2	Q8T4L8	Q8t4l8 drosoophila
1426	101	5.3	341	2	Q7KX22	Q7kx22	drosoophila	Q7kx22	drosoophila	1499	100.5	5.3	1503	2	Q7KT18	Q7kt18 drosoophila
1427	101	5.3	342	2	Q642G9	Q642g9	brachydanio	Q642g9	brachydanio	1500	100.5	5.3	1509	2	Q8IPG1	Q8ipg1 drosoophila
1428	101	5.3	344	2	Q91017	Q91017	caenorhabdi	Q91017	caenorhabdi							
1429	101	5.3	353	2	Q8MHQ3	Q8mhq3	gallus gall	Q8mhq3	gallus gall							
1430	101	5.3	391	2	Q7QJG1	Q7qjg1	anopheles g	Q7qjg1	anopheles g							
1431	101	5.3	532	2	Q6NNU3	Q6nnu3	drosoophila	Q6nnu3	drosoophila							
1432	101	5.3	532	2	Q9VLF0	Q9vlf0	drosoophila	Q9vlf0	drosoophila							
1433	101	5.3	606	2	Q61RH8	Q61rh8	rattus norv	Q61rh8	rattus norv							
1434	101	5.3	606	2	Q9ESS7	Q9ess7	mus musculus	Q9ess7	mus musculus							
1435	101	5.3	633	2	Q9VD13	Q9vd13	drosoophila	Q9vd13	drosoophila							
1436	101	5.3	648	2	Q9EPF1	Q9epf1	mus musculus	Q9epf1	mus musculus							
1437	101	5.3	648	2	Q8R2Y2	Q8r2y2	mus musculus	Q8r2y2	mus musculus							
1438	101	5.3	771	1	Q1GR_MOUSE	Q1gr_mouse	mus musculus	Q1gr_mouse	mus musculus							
1439	101	5.3	915	2	Q8R4B3	Q8r4b3	mus musculus	Q8r4b3	mus musculus							
1440	101	5.3	974	2	Q90777	Q90777	gallus gall	Q90777	gallus gall							
1441	101	5.3	976	2	Q9W755	Q9w755	brachydanio	Q9w755	brachydanio							
1442	101	5.3	1176	1	Q9W755	Q9w755	brachydanio	Q9w755	brachydanio							
1443	101	5.3	1210	1	Q9W755	Q9w755	brachydanio	Q9w755	brachydanio							
1444	101	5.3	1211	2	Q6LA76	Q6la76	homo sapien	Q6la76	homo sapien							
1445	101	5.3	1237	2	Q75147	Q75147	homo sapien	Q75147	homo sapien							
1446	101	5.3	1255	2	Q7Z329	Q7z329	homo sapien	Q7z329	homo sapien							
1447	101	5.3	1255	2	Q7YQL7	Q7yql7	pongo pygma	Q7yql7	pongo pygma							
1448	101	5.3	1255	2	Q7YQL8	Q7yql8	pan troglod	Q7yql8	pan troglod							
1449	101	5.3	1257	1	Q6ML_HUMAN	Q6ml_human	homo sapien	Q6ml_human	homo sapien							
1450	101	5.3	1578	2	Q76LL6	Q76ll6	mus musculus	Q76ll6	mus musculus							
1451	101	5.3	1723	2	Q8CHB2	Q8chb2	mus musculus	Q8chb2	mus musculus							
1452	101	5.3	2053	2	Q8WXU7	Q8wxu7	homo sapien	Q8wxu7	homo sapien							
1453	101	5.3	2092	2	Q76MU9	Q76mu9	homo sapien	Q76mu9	homo sapien							
1454	101	5.3	2113	2	Q8TDR4	Q8tdr4	homo sapien	Q8tdr4	homo sapien							
1455	101	5.3	4369	2	Q8MXD7	Q8mxd7	caenorhabdi	Q8mxd7	caenorhabdi							
1456	101	5.3	4650	2	Q15598	Q15598	homo sapien	Q15598	homo sapien							
1457	100.5	5.3	174	2	Q9GMZ9	Q9gmz9	felis silve	Q9gmz9	felis silve							
1458	100.5	5.3	201	2	Q9NBA9	Q9nba9	drosoophila	Q9nba9	drosoophila							
1459	100.5	5.3	212	2	Q9NBB0	Q9nbb0	drosoophila	Q9nbb0	drosoophila							
1460	100.5	5.3	235	2	Q6UWV2	Q6uwv2	homo sapien	Q6uwv2	homo sapien							
1461	100.5	5.3	245	1	Q6GFRAT	Q6gfrat	rattus norv	Q6gfrat	rattus norv							
1462	100.5	5.3	245	2	Q6MFX9	Q6mfx9	rattus norv	Q6mfx9	rattus norv							
1463	100.5	5.3	249	1	Q9P3A1	Q9p3a1	cricketul	Q9p3a1	cricketul							
1464	100.5	5.3	305	2	Q8VBW0	Q8vbw0	mus musculus	Q8vbw0	mus musculus							
1465	100.5	5.3	314	2	Q6X126	Q6x126	bovine herp	Q6x126	bovine herp							
1466	100.5	5.3	326	2	Q8UV70	Q8uv70	brachydanio	Q8uv70	brachydanio							
1467	100.5	5.3	332	2	Q95L16	Q95l16	felis silve	Q95l16	felis silve							
1468	100.5	5.3	335	1	Q9SG22	Q9sg22	homo sapien	Q9sg22	homo sapien							
1469	100.5	5.3	345	2	Q811H7	Q811h7	mus musculus	Q811h7	mus musculus							
1470	100.5	5.3	359	1	Q9HPL3	Q9hpl3	mouse	Q9hpl3	mouse							
1471	100.5	5.3	366	1	Q9HPL3	Q9hpl3	mouse	Q9hpl3	mouse							
1472	100.5	5.3	371	2	Q7Q127	Q7q127	anopheles g	Q7q127	anopheles g							
1473	100.5	5.3	413	2	Q9VAR6	Q9var6	drosoophila	Q9var6	drosoophila							
1474	100.5	5.3	440	2	Q9MK37	Q9mk37	macaca mula	Q9mk37	macaca mula							
1475	100.5	5.3	440	2	Q9MK38	Q9mk38	macaca mula	Q9mk38	macaca mula							
1476	100.5	5.3	449	2	Q9UE16	Q9ue16	homo sapien	Q9ue16	homo sapien							
1477	100.5	5.3	457	1	Q9D4_MOUSE	Q9d4_mouse	mus musculus	Q9d4_mouse	mus musculus							
1478	100.5	5.3	472	2	Q8P127	Q8p127	homo sapien	Q8p127	homo sapien							
1479	100.5	5.3	527	2	Q675X8	Q675x8	oikopleura	Q675x8	oikopleura							
1480	100.5	5.3	620	2	Q6UD74	Q6ud74	medicago tr	Q6ud74	medicago tr							
1481	100.5	5.3	708	1	Q9K1R2	Q9k1r2	homo sapien	Q9k1r2	homo sapien							
1482	100.5	5.3	719	1	Q9GROU_DROME	Q9grou_drome	drosoophila	Q9grou_drome	drosoophila							
1483	100.5	5.3	719	1	Q9GROU_DROME	Q9grou_drome	drosoophila	Q9grou_drome	drosoophila							
1484	100.5	5.3	730	2	Q7KRZ4	Q7krz4	drosoophila	Q7krz4	drosoophila							
1485	100.5	5.3	829	2	Q95KJ9	Q95kj9	macaca fasc	Q95kj9	macaca fasc							
1486	100.5	5.3	872	1	Q9CADI_XENLA	Q9cadi_xenla	xenopus lae	Q9cadi_xenla	xenopus lae							
1487	100.5	5.3	913	1	Q9B4L8_HUMAN	Q9b4l8_human	homo sapien	Q9b4l8_human	homo sapien							
1488	100.5	5.3	1026	2	Q7R0D0	Q7r0d0	giardia lam	Q7r0d0	giardia lam							
1489	100.5	5.3	1172	2	Q6ZRG7	Q6zrg7	homo sapien	Q6zrg7	homo sapien							
1490	100.5	5.3	1215	2	Q7KT17	Q7kt17	drosoophila	Q7kt17	drosoophila							
1491	100.5	5.3	1256	2	Q35158	Q35158	rattus norv	Q35158	rattus norv							

## ALIGNMENTS

## RESULT 1

Q9H6B4	PRELIMINARY;	PRT;	373 AA.
AC	Q9H6B4;		
DT	01-MAR-2001 (TRENBLrel. 16, Created)		
DT	25-OCT-2004 (TRENBLrel. 28, Last annotation update)		
DE	Hypothetical protein FLJ22415 (Adipocyte adhesion molecule)		
DE	(Adipocyte-specific adhesion molecule) (CAR-like membrane protein CLMP) (SLLL318).		
GN	Name=ASAM; Synonyms=CLMP; ORFNames=UNQ318;		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Kawabata A., Hiki T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,		
RA	Okitani R., Ota T., Suzuki Y., Ohayashi M., Nishi T., Shibahara T.,		
RA	Tanaka T., Nakamura Y., Isegai T., Sugano S.;		
RL	Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Eguchi J., Wada J., Hida K., Zhang H.;		
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Muscle;		
RX	MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Whiting J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RL	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Muscle;		
RA	Strausberg R.;		
RL	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		
RN	[5]		
RP	SEQUENCE FROM N.A.		
RX	PubMed=14573622; DOI=10.1074/jbc.M308249200;		
RA	Raschperger E., Engstrom U., Pettersson R.F., Fuxe J.;		
RT	"CLMP, a novel member of the CTX family and a new component of		

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RT epithelial tight junctions.":
RL J. Biol. Chem. 279:796-804(2004).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wiewand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AK026068; BAB15347.1; -
DR EMBL; AY264422; AAP88386.1; -
DR EMBL; BC009371; AAH09371.1; -
DR EMBL; AY358340; AAQ88706.1; -
DR EMBL; BK001245; DAA01139.1; -
DR HSSP; P78310; 1KAC.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
SQ SEQUENCE 373 AA; 41280 MW; FDA215EB3B3C4335 CRC64;

Query Match 100.0%; Score 1908; DB 2; Length 373;
Best Local Similarity 100.0%; Pred. No. 1.2e-123;
Matches 373; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSLLLLLLVSYVGTGLGTHTEIKRVAEEKVTLPCHHQGLGPEKDTLDIEWLLTDNEGNQ 60
Db 1 MSLLLLLLVSYVGTGLGTHTEIKRVAEEKVTLPCHHQGLGPEKDTLDIEWLLTDNEGNQ 60

Qy 61 KVVITYSRHRYNNLTTEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCVKNSGRYV 120
Db 61 KVVITYSRHRYNNLTTEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCVKNSGRYV 120

Qy 121 WSHVILKVLVRPSKPKCELEGELTEGSDLTLCQSSSGTEPIVYVQRIREKEGEDRLP 180
Db 121 WSHVILKVLVRPSKPKCELEGELTEGSDLTLCQSSSGTEPIVYVQRIREKEGEDRLP 180

Qy 181 PKSRIDYNHGKRVLLQNLTMYSGLYQCTAGNEAGKSCVVRVTQYVQSIGMVAGAVTG 240
Db 181 PKSRIDYNHGKRVLLQNLTMYSGLYQCTAGNEAGKSCVVRVTQYVQSIGMVAGAVTG 240

Qy 241 IVAGALLIFLLVLLIRRKDKERYEEERNEIREDAEAPKARLVKPSSSSGSRSSRS 300
Db 241 IVAGALLIFLLVLLIRRKDKERYEEERNEIREDAEAPKARLVKPSSSSGSRSSRS 300

Qy 301 SSSSTRSTANSASRSQRTLTSDAAPQGLATQAYSLVGPVGRGSEPKVHHANLTKAETTP 360
Db 301 SSSSTRSTANSASRSQRTLTSDAAPQGLATQAYSLVGPVGRGSEPKVHHANLTKAETTP 360

Qy 361 SMIPSQSRAFTQV 373
Db 361 SMIPSQSRAFTQV 373

RESULT 2
Q8K1G0 PRELIMINARY; PRT; 372 AA.
ID Q8K1G0
AC Q8K1G0;
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Adipocyte adhesion molecule.
GN Name=Acam;
OS Rattus norvegicus (Rat).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=OLET; TISSUE=Visceral adipose;
RA Hida K., Wada J., Zhang H., Makino H.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
EMBL; AF302047; AA076974.1; -
DR HSSP; P78310; 1KAC.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
SQ SEQUENCE 372 AA; 41148 MW; 439AB3C4D3E56346 CRC64;

Query Match 93.3%; Score 1781; DB 2; Length 372;
Best Local Similarity 93.2%; Pred. No. 6.9e-115;
Matches 345; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

Qy 4 LLLLLLVSYVGTGLGTHTEIKRVAEEKVTLPCHHQGLGPEKDTLDIEWLLTDNEGNQKV 63
Db 3 LFLVLVTVYVGTGLGTHTEIKRVAEEKVTLPCHHQGLGPEKDTLDIEWLLTDNEGNQKV 62

Qy 64 ITYSRRHRYNNLTTEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCVKNSGRYVWSH 123
Db 63 ITYSRRHRYNNLTTEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCVKNSGRYVWSH 122

Qy 124 VILKVLVRPSKPKCELEGELTEGSDLTLCQSSSGTEPIVYVQRIREKEGEDRLP 183
Db 123 VILKVLVRPSKPKCELEGELTEGSDLTLCQSSSGTEPIVYVQRIREKEGEDRLP 182

Qy 184 RIDYNHGKRVLLQNLTMYSGLYQCTAGNEAGKSCVVRVTQYVQSIGMVAGAVTGIVA 243
Db 183 RIDYNHGKRVLLQNLTMYSGLYQCTAGNEAGKSCVVRVTQYVQSIGMVAGAVTGIVA 242

Qy 244 GALLIFLLVLLIRRKDKERYEEERNEIREDAEAPKARLVKPSSSSGSRSSRS 303
Db 243 GALLIFLLVLLIRRKDKERYEEERNEIREDAEAPKARLVKPSSSSGSRSSRS 302

Qy 304 TRSTANSASRSQRTLTSDAAPQGLATQAYSLVGPVGRGSEPKVHHANLTKAETTPSI 363
Db 303 TRSTANSASRSQRTLTSDAAPQGLATQAYSLVGPVGRGSEPKVHHANLTKAETTPSI 362

Qy 364 PSQSRFAFTQV 373
Db 363 PSQSRFAFTQV 372

RESULT 3
Q8R373 PRELIMINARY; PRT; 373 AA.
ID Q8R373
AC Q8R373;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE CAR-like membrane protein (Adipocyte adhesion molecule) (Mus musculus
DE adult male cecum cDNA, RIKEN full-length enriched library.
DE clone:9130232017 product:ADIPOCYTE-SPECIFIC PROTEIN 5, full insert
DE sequence).
GN Name=9030425E11rik; Synonyms=CLMP;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=FVB/N; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Klausner S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Blakesley A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor;  
 RA Strausberg R.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Swiss Webster;  
 RA Eguchi J., Wada J., Hida K., Zhang H.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cecum;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cecum;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cecum;  
 RA The FANTOM Consortium,  
 RT the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RA "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 [7]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cecum;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayateu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 [8]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cecum;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shabata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 [9]  
 RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cecum;  
 RA Adachi J., Furuno K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 [10]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Swiss webster/NIH;  
 RX PubMed=14573622; DOI=10.1074/jbc.M308249200;  
 RA Raschperger E., Engstrom U., Pettersson R.F., Fuxe J.;  
 RT "CLMP, a novel member of the CTX family and a new component of  
 epithelial tight junctions.";  
 RL J. Biol. Chem. 279:796-804(2004).  
 DR EMBL; BC026447; AAH26447.1; -  
 DR EMBL; AY326421; AAP88385.1; -  
 DR EMBL; AK033723; BAC28446.1; -  
 DR EMBL; AY259213; AAP15240.1; -  
 DR HSSP; F78310; IKAC.  
 DR MGD; MGI:1918816; 9030425E11rik.  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR GO; GO:0016021; C:integral to membrane; TAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003598; IG\_C2.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00408; IGC2; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 2.  
 SQ SEQUENCE 373 AA; 41214 MW; 9C6288484AF95512 CRC64;  
 Query Match 92.4%; Score 1763.5; DB 2; Length 373;  
 Best Local Similarity 92.7%; Pred. No. 1.le-113;  
 Matches 344; Conservative 12; Mismatches 14; Indels 1; Gaps 1;  
 QY 4 LLLLLVSYVYVGTGTHTEIKRVAEKKVTLPCHQGLGPEKDTLDIEWLLTDNEGKQKV 63  
 DB 3 LFFLWLSVYVGTGTHTEIKRVAEKKVTLPCHQGLGPEKDTLDIEWLLTDNEGKQKV 62  
 QY 64 ITYSRHHVNNLTTEEQGRVAFASNFLAGDASLQIEPLKPSDEGRYTCVKNSGRYVWSH 123  
 DB 63 ITYSRHHVNNLTTEEQGRVAFASNFLAGDASLQIEPLKPSDEGRYTCVKNSGRYVWSH 122  
 QY 124 VILKVLVRPSKPKCELEGELTEGSDTLTQCSSSGTEPIVYVWQIRKEGEDEHLPPKS 183  
 DB 123 VILKVLVRPSKPKCELEGEPTEGSDTLTQCSSASGTPIVYVWQIRKEGEDEHLPPKS 182  
 QY 184 RIDYNHPRVLLQNLTWSSGLYOCAGNEAGKSCVVRVTQVQVQSIGMVAGAVTGIVA 243  
 DB 183 RIDYNHPRVLLQNLTWSSGLYOCAGNEAGKSCVVRVTQVQVQSIGMVAGAVTGIVA 242  
 QY 244 GALLIFLLVWLLIRKKERYEEERPNIEDEAPKARLVKPPSSSSSGSSSSSSSSSS 303  
 DB 243 GALLIFLLVWLLIRKKERYEEERPNIEDEAPKARLVKPPSSSSSGSSSSSSSSSS 302  
 QY 304 TRSTANGASRSQRTLSLTDAP-QGLATQAVSLVGVGEVPSGPKVHHANLTKATTTSM 362  
 DB 303 TRSTGNSASRSQRTLSLSEAPQGLAPQAVSLIGPEVRGSEPKVHHHTLTTLTKAETTLST 362  
 QY 363 IPSOSRAPOTV 373  
 DB 363 TPSQSKAPQTV 373  
 RESULT 4  
 Q92055  
 ID Q92055 PRELIMINARY; PRT; 373 AA.  
 AC Q92055;



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DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Adipocyte-specific protein 5.
GN Name=9030425E11rik; Synonyms=asp5;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB040490; BAB58503.1; -.
DR HSSP; P78310; IKAC.
DR MGD; MGI:1918816; 9030425E11rik.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
SQ SEQUENCE 373 AA; 41186 MW; 5C6280584AF95326 CRC64;

Query Match 92.2%; Score 1759.5; DB 2; Length 373;
Best Local Similarity 92.5%; Pred. No. 2.1e-113;
Matches 343; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

QY 4 LLLLLLVSYVGTGLTHTTEIKRVAEEKVTLPCCHQLGLPEKDTLDIEWLLTDNEGKQV 63
DB 3 LFFLWLVSYYVGTGLTHTTEIKRVAEEKVTLPCCHQLGLPEKDTLDIEWLLTDNEGKQV 62
QY 64 ITYSRRHYNNLTBEOKGRVAFASFLAGDASLOIEPLKPSDEGRYTCKVNSGRYVWSH 123
DB 63 ITYSRRHYNNLTBEOKGRVAFASFLAGDASLOIEPLKPSDEGRYTCKVNSGRYVWSH 122
QY 124 VILKVLVRPSKPKCELEGELTEGSDLTLCQSSSGTEPIVYVQRIREKEGEDRLPPKS 183
DB 123 VILKALVRPSKPKCELEGTEGSDLTLCQSSSGTEPIVYVQRIREKEGEDRLPPKS 182
QY 184 RIDYVHGRVLLQNLTMSSGLYQCTAGNEAGKSCVVRVTQVYVQSIGMVAGAVTGIVA 243
DB 183 RIDYVHGRVLLQNLTMSSGLYQCTAGNEAGKSCVVRVTQVYVQSIGMVAGAVTGIVA 242
QY 244 CALLIFLVLIRRKDKRYEEREPNEIREDAEAPKARLVKPSSSSGSSRSRSGSS 303
DB 243 CALLIFLVLIRRKDKRYEEREPNEIREDAEAPKARLVKPSSSSGSSRSRSGSS 302
QY 304 TRSTANSASRSQRTLTSDAAP--QPGLAQVSLVGPVGRSEPKKVHHANLTKAETTPSM 362
DB 303 TRSTGNSASRSQRTLTSSAAAPQPGFGLAQVSLVGPVGRSEPKKVHHANLTKAETTLST 362
QY 363 IPSQSRAFQTV 373
DB 363 TPSQSAFQTV 373

RESULT 5
Q640U3 PRELIMINARY; PRT; 332 AA.
AC Q640U3;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RL TISSUE=Whole body;
RC PubMed=12477932; DOI=10.1073/pnas.242603899;
RX
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner F.S., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.B., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RA Klein S., Gerhard D.S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC082496; AAH82496.1; -.
KW Hypothetical protein.
SQ SEQUENCE 332 AA; 36851 MW; 0DF9DEB7D4BB426C CRC64;

Query Match 41.3%; Score 787.5; DB 2; Length 332;
Best Local Similarity 51.1%; Pred. No. 2.4e-46;
Matches 165; Conservative 51; Mismatches 102; Indels 5; Gaps 3;

QY 2 SLLLLLVSYVGTGLTHTTEIKRVAEEKVTLPCCHQLGLPEKDTLDIEWLLTDNEGKQ 61
DB 3 TLIRSLGLMWVLGAL-AQTEIKLVADENVTLPCRSLHGLIOSLDIEWLSNISHGKQ 61
QY 62 VVIYSSRRHYNNLTBEOKGRVAFASFLAGDASLOIEPLKPSDEGRYTCKVNSGRYVW 121
DB 62 VLLSYSGGVVN--AENHKGRYSFVKYLEGDASLFRSLQPSDAGQYICKVKNAGQYQW 119
QY 122 SHVILKVLVRPSKPKCELEGELTEGSDLTLCQSSSGTEPIVYVQRIREKEGEDRLPP 181
DB 120 SFITIVILVKPSELACSSGAQLEGKVTNCKTAGTKPLNVRVVRVNLNDVPERPVS 179
QY 182 KSRIDYVHGRVLLQNLTMSSGLYQCTAGNEAGKSCVVRVTQVYVQSIGMVAGAVTG 241
DB 180 TARI--GPNQLLHNLKTDNGSYRCEVSNVEGKRTCDVDVTQVSVNTGLAGVACGV 237
QY 242 VAGALLIFLVLIRRKDKRYEEREPNEIREDAEAPKARLVKPSSSSGSSRSRSGS 301
DB 238 VGVFLIFFTVLLFHKKFKEFKREBEFFNEIREDAEAPKARLVKPSGSSSDSRSSQSGS 297
QY 302 SSTRSTANSASRSQRTLTSDAAP 324
DB 298 SSTRSTNSASRSQRTHTSTQETP 320

RESULT 6
Q8C1H8 PRELIMINARY; PRT; 160 AA.
AC Q8C1H8;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DE 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Mus musculus adult male colon cDNA, RIKEN full-length enriched
DE library, clone:9030425E11 product:ADIPOCYTE-SPECIFIC PROTEIN 5, full
DE insert sequence. (Fragment).
GN Name=9030425E11rik;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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QY	112	KVXNSGRVW	SHVILKVL	VRPSKPKC	ELGEGELTE	GSDDLTLQ	CESSSGTEP	IVYVQRI	RE	171	
DB	121	KVKAPGVGN	KKIQLTVL	VKPSGIRC	VDSBEEIGN	DFLKECP	EGSLPLAYE	QOKL--		178	
QY	172	KEGEDERLP	PKSRIDYNH	PORVLLON	TMSYSGLY	OCTAGNEA	GKESCVCVR	V--TVQYV	QS	230	
DB	179	--SDSQKL	PTSWLP	EMTSP--	VISVKNA	ASAEYS	TYTCTV	RNRVGS	QOCLRLD	VVP	235
QY	231	IGWAGAVT	GIVAGALLI	FLVWLLIR	RKKDKE	RYEEER	PNETREDA	EAPKARL	VKPS	290	
DB	236	AGTIAGAV	IGTLLALV	LIALIVFC	CHKRRE	EYKEVH--	HDIREV	DPVPK	SRTST	ARS	294
QY	291	SGSRSRSG	SGSSTST	ANSASORT	LSTD--	AAPO--	PGLATQ	AYSLV	GPEVRG	SEPK	347
DB	295	IGSNHSS	LGMS	PMNMEG	YSKTQNV	QVPS	EDLEAP	QSP	PTL-----	PPAK	339
QY	348	VHANLTK	ATKAT	TPPSMP	ISQSR	368					
DB	340	VAAPNLS	SRMGAV	VPVMI	PAQSK	360					

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97190109; PubMed=9036860; DOI=10.1126/science.275.5304.1320;  
RA Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,  
RA Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;  
RT "Isolation of a common receptor for Coxsackie B viruses and  
RT adenoviruses 2 and 5.";  
RL Science 275:1320-1323 (1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97250541; PubMed=9096397; DOI=10.1073/pnas.94.7.3352;  
RA Tomko R.P., Xu R., Philipson L.;  
RT "HCAR and MCAR, the human and mouse cellular receptors for subgroup C  
RT adenoviruses and group B coxsackieviruses";  
RL Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356 (1997).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=2008750; PubMed=10543405;  
RA Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A., Bowles N.E.;  
RT "Genomic organization and chromosomal localization of the human  
RT coxsackievirus B-adenovirus receptor gene.";  
RL Hum. Genet. 105:354-359 (1999).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX Anderson C.W., Kieleczawa J., Dunn J.J., Freimuth P.;  
RT "Sequence and expression of CXADR, the human gene for the  
RT coxsackievirus and adenovirus receptor.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBAJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RX Andersson B., Tomko R., Andersson K., Darban H., Oncu D., Mizra M.,  
RA Sollerbrant K., Sonnenhammer E., Philipson L.;  
RT "Putative regulatory domains in the human and mouse CAR genes.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBAJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Cervix;  
RP RC

RT coxsackievirus and adenovirus receptor.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RA Andersson B., Tomko R., Andersson K., Darban H., Oncu D., Mizra M.,  
RA Sollerbrant K., Sonhammer E., Philipson L.;  
RT "Putative regulatory domains in the human and mouse CAR genes.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Cervix;

RX MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;  
 RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Pahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RL subgroups C of adenoviruses (AD2 and AD5).  
 CC -!- FUNCTION: Serves as a receptor for group B coxsackieviruses and  
 CC subgroups C of adenoviruses (AD2 and AD5).  
 CC -!- SURCELLULAR LOCATION: Type 1 membrane protein.  
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC  
 DR EMBL; Y07593; CAA68868.1; -;  
 DR EMBL; U0716; AAC5124.1; -;  
 DR EMBL; AF169366; AAF05908.1; JOINED.  
 DR EMBL; AF169361; AAF05908.1; JOINED.  
 DR EMBL; AF169362; AAF05908.1; JOINED.  
 DR EMBL; AF169363; AAF05908.1; JOINED.  
 DR EMBL; AF169364; AAF05908.1; JOINED.  
 DR EMBL; AF169365; AAF05908.1; JOINED.  
 DR EMBL; AF200465; AAF24344.1; -;  
 DR EMBL; AF242865; AAG01088.1; JOINED.  
 DR EMBL; AF242862; AAG01088.1; JOINED.  
 DR EMBL; AF242864; AAG01088.1; JOINED.  
 DR EMBL; BC03684; AAH03684.1; -;  
 DR EMBL; BC010536; AAH0536.1; -;  
 DR PDB; 1EAB; X-ray; A/B=15-140.  
 DR PDB; 1F5W; X-ray; A/B=15-140.  
 DR PDB; 1KAC; X-ray; B=21-144.  
 DR Genew; HGNC:2559; CXADR.  
 DR H-InvdB; HIX0016031; -;  
 DR MIM; 602621; -;  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0004872; F:receptor activity; TAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003598; Ig\_C2.  
 DR Pfam; PF00047; Ig; 2.  
 DR SMART; SM00408; IGC2; 1.  
 DR PROSITE; PS0835; IG\_LIKE; 2.  
 DR 3D-structure; Glycoprotein; Immunoglobulin domain; Receptor; Repeat;  
 KW Signal; Transmembrane.  
 FT SIGNAL 1 19  
 FT CHAIN 20 365  
 FT DOMAIN 20 237  
 FT TRANSMEM 238 258  
 FT DOMAIN 259 365  
 FT DOMAIN 20 134  
 FT DOMAIN 141 228  
 FT DOMAIN 41 120  
 FT DISULFID 162 212  
 FT By similarity.

FT CARBOHYD 106 106 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 201 201 N-linked (GlcNAc...) (Potential).  
 FT STRAND 21 22  
 FT STRAND 27 32  
 FT TURN 33 34  
 FT STRAND 37 39  
 FT STRAND 42 44  
 FT TURN 47 48  
 FT STRAND 53 61  
 FT TURN 62 63  
 FT STRAND 69 75  
 FT TURN 76 77  
 FT STRAND 78 80  
 FT TURN 82 83  
 FT STRAND 86 90  
 FT TURN 91 93  
 FT HELIX 98 100  
 FT TURN 101 101  
 FT STRAND 102 102  
 FT STRAND 105 107  
 FT HELIX 112 114  
 FT STRAND 116 124  
 FT TURN 125 126  
 FT STRAND 127 138  
 SQ SEQUENCE 365 AA; 40029 MW; AB01C6346CB7FE64 CRC64;  
 Query Match 24.4%; Score 465; DB 1; Length 365;  
 Best Local Similarity 31.6%; Pred. No. 5e-24;  
 Matches 122; Conservative 69; Mismatches 151; Indels 44; Gaps 9;  
 QY 1 MSLLLLLLLVYVG-----TLGTHTR-IKRVAEKVTLPCHHQGLGPEKOTLDIEWLLT 54  
 DB 1 MALLLCFVLLCGVDFARSLSTITPEEMIEKAKGETAYLPCKFTLSPEQDGLDIEWLLS 60  
 QY 55 --DREGNCKVITVSSRHVYNNLTTEEOKRVAFASNFL-AGDASLQIPLKPSDSGRYTC 111  
 DB 61 PADNQKVDQVILYSGDKYDDYDPLDKRGVHFTSNDLKSGDASINVNLQSLDGTQYC 120  
 QY 112 KVNQSGRYVWSHVILKLVPRSPKCELEGELTEGSDLTLCQESSSGTEPIVYVYQRIRE 171  
 DB 121 KVKKAPGVANKKIHLVLPKPGARCYDVGSEIGDFKICEPKESGSLPQYEWQKL-- 178  
 QY 172 KEGDERLPKSRIDYNHGVRVLLQNLVMSYGLYQCTAGNEAGKESCVRV-TVQYVOS 230  
 DB 179 --SDSQKPTSWLAEMTSSTVISVKNASSEYSGTYSCTVRNRVGDQCLLRNLVVPSPNK 235  
 QY 231 IGMVAGAVTGIVAGALLIFLLVLLIRKDKERYEEERPNREDAEAPKARL----- 284  
 DB 236 AGLIAGAIIGTLLALALIGLIIFCCRKRRBEKYEKVH-HDIREDPVPPKSTRTARSY 294  
 QY 285 --VKPSSSSGSRSSRSGSSSTRSTANSASRSQRTLSLTDAAAPQGLATQAVSLVGPEVRG 342  
 DB 295 IGSNHSLSGMSPSNMEGYSKTQYNQVSEDFERTPQSTLP----- 336  
 QY 343 SEPKKVHHANLTAKAETTPSMIPQSQR 368  
 DB 337 --PAKVAAPNLSRMGAIPVMIPAQSK 360  
 RESULT 10  
 Q9R066 PRELIMINARY; PRT; 358 AA.  
 ID Q9R066  
 AC Q9R066;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Cxsackie-adenovirus-receptor homolog (Fragment).  
 GN Name=CAR1;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]



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QY 175 EDERLPKSRIDYHNPGRVLLQNLTMYSGLYQCTAGNEAGKESCVVRV-TVQYVQSIGM 233
DB 180 DSQTMPTWLAEMTSP-VISVKNASSEYSGTYSCTQNRVSGDQCWLRLDVVPPNRACT 238
QY 234 VAGAVTGVAGALLIFLLVLLIRKDKERYEERNEIREDAEPKARLVKPPSSSSG 293
DB 239 IAGAVIGTLLALVLGAILFCCHRRKREKEVH-HDIREDDVPPPKSRSTARSYIGS 297
QY 294 SRSSRSGSSTRSTANSASRSQRTLSTD--AAPO-PGLATQAYSLVGPVEVRGSEPKVHH 350
DB 298 NHSSLSGMSPSNMEGYSKTYQNVPSDFERAPQSTLA-----PAKVAA 342
QY 351 ANLTKAETTPSMIPQSR 368
DB 343 PNLRMGAVPVMPAQSK 360

RESULT 12
Q9DBJ8 PRELIMINARY; PRT; 365 AA.
AC Q9DBJ8
DB Q9DBJ8
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DE Mus musculus adult male liver cDNA, RIKEN full-length enriched
DE library, clone:1300005A16 product:coxsaackievirus and adenovirus
DE receptor, full insert sequence.
GN Name=Cxadr;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=92279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa K., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
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RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito K., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Segabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK004908; BAB23660.2; -.
DR HSSP; P78310; IKAC.
DR MGD; MGI:1201679; Cxadr.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Receptor.
SQ SEQUENCE 365 AA; 39947 MW; 5445B4B52A34B2A2 CRC64;

Query Match 24.0%; Score 457.5; DB 2; Length 365;
Best Local Similarity 32.0%; Pred. No. 1.6e-23;
Matches 121; Conservative 70; Mismatches 154; Indels 33; Gaps 11;

QY 3 LLLLLL--VSYYVYGLTGHTTEIKRVAE---EKTLPCHHQLGLPEKDTLDLWLL--TD 55
DB 4 LLCVLLCGIADFTSGLSITTPQRIEKAKGETAYLPCKFTLSPDQGPLDIWLIISPD 63
QY 56 NEGKQKVITYSSRHVYNNLTETEEQKRVAFASNFL-AGDASLIQIEPLKPSDEGRYTCVK 114
DB 64 NQIVDQVILYSGDKIYDNYVYPLKGRVHFTSNDVKSGDASINVTNLQSLDGTGYCKVK 123
QY 115 NSGRYVNSHVILKVLVRPSKPKCELEGELTSGSLDTLQCESSSGTEPIVYVQRTREK 174
DB 124 KAPGVANKFLLTLVLVPSGTRCFVDGSEELGNDPKLCEPKESLPLQFENQKL----S 179
QY 175 EDERLPKSRIDYHNPGRVLLQNLTMYSGLYQCTAGNEAGKESCVVRV-TVQYVQSIGM 233
DB 180 DSQTMPTWLAEMTSP-VISVKNASSEYSGTYSCTQNRVSGDQCWLRLDVVPPNRACT 238
QY 234 VAGAVTGVAGALLIFLLVLLIRKDKERYEERNEIREDAEPKARLVKPPSSSSG 293
DB 239 IAGAVIGTLLALVLGAILFCCHRRKREKEVH-HDIREDDVPPPKSRSTARSYIGS 297
QY 294 SRSSRSGSSTRSTANSASRSQRTLSTD--AAPO-PGLATQAYSLVGPVEVRGSEPKVHH 350
DB 298 NHSSLSGMSPSNMEGYSKTYQNVPSDFERAPQSTLA-----PAKVAA 342
QY 351 ANLTKAETTPSMIPQSR 368
DB 343 PNLRMGAVPVMPAQSK 360

RESULT 13
Q9TU79 PRELIMINARY; PRT; 319 AA.
AC Q9TU79
DB Q9TU79
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE Coxsackie-adenovirus-receptor homolog (Fragment).
GN Name=CAR;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=99422053; PubMed=10490761;
RA Fechner H., Haack A., Wang H., Wang X., Eizema K., Pauschinger M.,
RA Schoemaker R.G., van Veghel R., Houtsmuller A.B., Schultheiss H.-P.,
RA Lamers J.M.J., Poller W.;
RA "Expression of Coxackie-adenovirus-receptor and alpha v-integrin does
RT not correlate with adenovector targeting in vivo indicating anatomical
RT vector barriers.";
RT Gene Ther. 6:1520-1535 (1999).
RL EMBL; AF109646; AAF01257.1; -.
DR HSSP; P78310; IKAC.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Receptor.
FT NON TER 319 319
SQ SEQUENCE 319 AA; C485555A6C9F1B5B CRC64;

Query Match 23.2%; Score 443; DB 2; Length 319;
Best Local Similarity 35.1%; Pred. No. 1.4e-22;
Matches 114; Conservative 63; Mismatches 130; Indels 18; Gaps 10;

QY 1 MSLLVSYVCTLGTHTE---IKVAEKEVTLPCGHQGLPEKDTLDIEWLLT 54
DB 1 MALLRFVLLCGVADLTSLTSITTPQMIKAKGTAYLPCKFTLSPEDQGPLDIWLLS 60

QY 55 --DNEGQKVVTYSSRHVYNNLTTEEOKGRVAFASNFL-AGDASLQIEPLKPSDEGRYTC 111
DB 61 PADNQKVDQVILYSGDKIYDDYDYLKGRVHFTSNLKGSDASINVTNLQSLDGTGYQC 120

QY 112 KVNKSGRYVWSHVILKVLVRSPKPCLEBELTSGSDLTLOCESSSGTEPIVYVQWIRE 171
DB 121 KVKAPGVGNKKIQLTVLLKPSGTCTCYDGSSEIGNDPKLCEPKEGSLPLLYEQWL-- 178

QY 172 KEGEDERLPKRSRIDYNHGPRVLLQNLTMVSYGLYQCTAGNEAGKESCVRV-TVQYVQS 230
DB 179 --SNSQKPLTLWAEWTFP-VISVKNASTESVGTCTVKNRVSQDQCLLRDLVPPSNR 235

QY 231 IGMVAGAVTGVAGALLIFLLVWLLIRKDKERYEEERPNIEIRDAEAPKARLVPKPS 290
DB 236 AGTIAGAVIGVLLALVLIIFCCKRREKEVH-HDIREDDVPPKSR-TSTARS 293

QY 291 SSGSRSSRSSTSTANSASRSQ 315
DB 294 YLGSNHSLSGMSNP-SNMEGYSKTQ 317

RESULT 14
Q9UKV4 PRELIMINARY; PRT; 344 AA.
AC Q9UKV4;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Coxackie and adenovirus receptor protein (Fragment).
GN Name=HCAR2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=99422053; PubMed=10490761;
RA Fechner H., Haack A., Wang H., Wang X., Eizema K., Pauschinger M.,
RA Schoemaker R.G., van Veghel R., Houtsmuller A.B., Schultheiss H.-P.,
RA Lamers J.M.J., Poller W.;
RA "Expression of Coxackie-adenovirus-receptor and alpha v-integrin does
RT not correlate with adenovector targeting in vivo indicating anatomical
RT vector barriers.";
RT Gene Ther. 6:1520-1535 (1999).
RL EMBL; AF109643; AAF01254.1; -.
DR HSSP; P78310; IKAC.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
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RT "Expression of Coxackie-adenovirus-receptor and alpha v-integrin does
RT not correlate with adenovector targeting in vivo indicating anatomical
RT vector barriers.";
RL Gene Ther. 6:1520-1535 (1999).
DR EMBL; AF124598; AAD31172.1; -.
DR HSSP; P78310; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Receptor.
FT NON TER 344 344
SQ SEQUENCE 344 AA; 38097 MW; BEF3722B96C697AA CRC64;

Query Match 22.8%; Score 434.5; DB 2; Length 344;
Best Local Similarity 32.5%; Pred. No. 5.9e-22;
Matches 114; Conservative 65; Mismatches 147; Indels 25; Gaps 9;

QY 1 MSLLLLLLVSYVVG---TLGTHTE-IKVAEKEVTLPCGHQGLPEKDTLDIEWLLT 54
DB 1 MALLLCFVLLCGVVDVFARSLSTTPPEMIEKAKGTAYLPCKFTLSPEDQGPLDIWLLS 60

QY 55 --DNEGQKVVTYSSRHVYNNLTTEEOKGRVAFASNFL-AGDASLQIEPLKPSDEGRYTC 111
DB 61 PADNQKVDQVILYSGDKIYDDYDYLKGRVHFTSNLKGSDASINVTNLQSLDGTGYQC 120

QY 112 KVNKSGRYVWSHVILKVLVRSPKPCLEBELTSGSDLTLOCESSSGTEPIVYVQWIRE 171
DB 121 KVKAPGVGNKKIHLVVLVLPKPGARCYVDGSSEIGSDPKICEPKEGSLPLQYEQWL-- 178

QY 172 KEGEDERLPKRSRIDYNHGPRVLLQNLTMVSYGLYQCTAGNEAGKESCVRV-TVQYVQS 230
DB 179 --SDSQMPTSLWAEWTFP-VISVKNASTESVGTCTVKNRVSQDQCLLRDLVPPSNK 235

QY 231 IGMVAGAVTGVAGALLIFLLVWLLIRKDKERYEEERPNIEIRDAEAPKARL----- 284
DB 236 AGLIAGAIIGTLLALALIGLIIFCCKRREKEVH-HDIREDDVPPKSR-TSTARS 294

QY 285 --VFPSSSSRSRSGSSSTSTANSASRSQTLSTDAAPQCLATQAY 333
DB 295 IGSNHSLSGMSNP-SNMEGYSKTQYNQVPSDFERTPQSTLTP-PAKFKYAY 344

RESULT 15
Q9R067 PRELIMINARY; PRT; 344 AA.
AC Q9R067;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Coxackie-adenovirus-receptor homolog (Fragment).
GN Name=CAR2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=99422053; PubMed=10490761;
RA Fechner H., Haack A., Wang H., Wang X., Eizema K., Pauschinger M.,
RA Schoemaker R.G., van Veghel R., Houtsmuller A.B., Schultheiss H.-P.,
RA Lamers J.M.J., Poller W.;
RA "Expression of Coxackie-adenovirus-receptor and alpha v-integrin does
RT not correlate with adenovector targeting in vivo indicating anatomical
RT vector barriers.";
RT Gene Ther. 6:1520-1535 (1999).
RL EMBL; AF109643; AAF01254.1; -.
DR HSSP; P78310; IKAC.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
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DR SMART: SM00408; IGC2: 1.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
KW Receptor.  
FT. NON\_TER 344 344  
SQ SEQUENCE 344 AA; 38030 MW; D436498820D8B9B7 CRC64;

Query Match 22.7%; Score 433.5; DB 2; Length 344;  
Best Local Similarity 32.7%; Pred. No. 6.9e-22;  
Matches 112; Conservative 68; Mismatches 143; Indels 19; Gaps 10;

QY	1	MSLLILLLL--VSYVVGTLGTHTEIKRVAE---EKVTLPCHHQLGLPEKDTLDIEWLL-	53
DB	1	MALLLCFVLLCGVADFTSSLSITTPQRIEKAKGETAYLPCKFTLEPEDQGPLDIEWLLS	60
QY	54	-TDNEGNQKVITYSSRRHYNNLTREQKGRVAPASNFL-AGDASLQIEPLKPSDEGRYTC	111
DB	61	PSDNQKVDQVILLYSGDKIYDNYYPDLKGRVHFTSNDVKSGDASINVTNLQLSDIGTYQC	120
QY	112	KVNSGRVYVSHVILKVLVYRPSKPCLEGEELTEGSDLTLOCESSSGTEPIVYVWQRIRE	171
DB	121	KVKKAPGVANRXFLTLVLPKPGTCFVDSGGEIGNDFKLKCEPKEGSLPQYEWQKL--	178
QY	172	KEGEDERLPKSRIDYNHPCRVLLQNLTWISGLYQCTAGNEAGKESCVRV-TVQYVQS	230
DB	179	--SDSQKMTPLWLAETSP-VISVKNASSEYSGTYSCTVQNRVGSQCMRLDVPVPSNR	235
QY	231	IGWVAGAVTGIVAGALLIFLLVLLIRRKDKERYEEERPNREIREDAEAPKARLVKPSSS	290
DB	236	AGTIAGAVIGTLLALVLIGAILFCCHKRREKEKEVH-HDIREDVPPPKSRTSTARSY	294
QY	291	SSGSRSSRSRSGSSSTRSTANSASRSQRTLSTD--AAPQ-PGLA	329
DB	295	IGSNHSSLGSMSPSNMEGYSKTQYNQVPSDFERAPQSPTLA	336

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Job time : 215 secs

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